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## OM protein - protein search, using sw model

Run on: May 2, 2002, 08:48:18 ; Search time 12.56 Seconds

(without alignments)  
576,916 Million cell updates/sec

Title: US-09-823-038a-33

Perfect score: 1779  
Sequence: 1 RRAPCCSCRCRCGMPGSHR.....VLPTGDVMSRPDGSYLNRPL 322

## Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

## Database :

1: /cgcn2\_6/ptodata/2/1aa/5A.COMB.pep.\*  
2: /cgcn2\_6/ptodata/2/1aa/5B.COMB.pep.\*  
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6: /cgcn2\_6/ptodata/2/1aa/backfile1a1.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	1779	100.0	322 4 US-09-383-586-33	Sequence 33, Appl
2	1371	77.1	529 4 US-09-383-586-31	Sequence 31, Appl
3	1029	57.8	439 4 US-09-383-586-32	Sequence 32, Appl
4	391	22.0	801 4 US-09-383-630-6	Sequence 6, Appl
5	378	21.2	806 4 US-09-383-630-3	Sequence 3, Appl
6	375.5	21.1	335 1 US-08-471-570-14	Sequence 14, Appl
7	375.5	21.1	643 1 US-08-471-570-6	Sequence 6, Appl
8	375.5	21.0	769 1 US-08-471-570-8	Sequence 8, Appl
9	373	21.0	816 1 US-07-640-029-1	Sequence 1, Appl
10	371.5	20.9	821 2 US-08-451-822A-13	Sequence 13, Appl
11	364.5	20.5	820 1 US-07-921-807B-3	Sequence 3, Appl
12	364.5	20.5	820 1 US-08-441-944A-3	Sequence 3, Appl
13	364.5	20.5	820 1 US-08-439-992A-1	Sequence 1, Appl
14	360.5	20.3	351 5 PCT-US93-05703-2	Sequence 2, Appl
15	360.5	20.3	817 1 US-07-640-029-2	Sequence 2, Appl
16	360.5	20.3	822 1 US-07-921-807B-4	Sequence 4, Appl
17	360.5	20.3	822 1 US-08-459-286-2	Sequence 2, Appl
18	360.5	20.3	822 1 US-08-441-944A-4	Sequence 4, Appl
19	360.5	20.3	822 4 US-08-451-822A-12	Sequence 12, Appl
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21	359.5	20.2	822 1 US-07-997-133-1	Sequence 1, Appl
22	350	19.7	126 4 US-09-383-586-30	Sequence 30, Appl
23	349.5	19.6	820 1 US-08-166-717D-6	Sequence 6, Appl
24	308	17.3	300 1 US-07-640-029-5	Sequence 5, Appl
25	308	17.3	300 4 US-08-439-992A-5	Sequence 5, Appl
26	307	17.3	526 1 US-08-471-570-4	Sequence 4, Appl
27	307	17.3	652 1 US-08-471-570-10	Sequence 10, Appl

28	306	17.2	302 1 US-07-921-807B-7	Sequence 7, Appl
29	306	17.2	302 1 US-08-441-944A-7	Sequence 7, Appl
30	305	17.1	240 1 US-08-471-570-12	Sequence 12, Appl
31	304	17.1	302 1 US-07-640-029-6	Sequence 6, Appl
32	304	17.1	302 1 US-07-921-807B-8	Sequence 8, Appl
33	304	17.1	302 1 US-08-441-944A-8	Sequence 8, Appl
34	304	17.1	302 4 US-08-439-992A-6	Sequence 6, Appl
35	304	17.1	731 1 US-07-921-807B-5	Sequence 5, Appl
36	304	17.1	731 1 US-08-441-944A-5	Sequence 5, Appl
37	304	17.1	733 1 US-08-439-992A-3	Sequence 3, Appl
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40	304	17.1	733 1 US-08-471-570-10	Sequence 10, Appl
41	304	17.1	733 4 US-08-439-992A-4	Sequence 4, Appl
42	301	16.9	729 1 US-07-640-029-3	Sequence 3, Appl
43	282.5	15.9	729 1 US-08-070-165F-6	Sequence 6, Appl
44	282.5	15.9	729 2 US-08-885-418-6	Sequence 6, Appl
45	282.5	15.9	731 1 US-08-070-165F-10	Sequence 10, Appl
46	282.5	15.9	731 2 US-08-885-418-10	Sequence 10, Appl
47	237	13.3	1651 4 US-09-540-245A-18	Sequence 18, Appl
48	234.5	13.2	1101 3 US-08-986-465-2	Sequence 2, Appl
49	233	13.1	1297 4 US-09-540-245A-17	Sequence 17, Appl
50	233	13.1	1395 4 US-09-540-245A-15	Sequence 15, Appl
51	230.5	13.0	946 5 PCT-US95-08493-13	Sequence 13, Appl
52	228	12.8	1381 4 US-09-540-245A-16	Sequence 16, Appl
53	225	12.6	615 2 US-08-752-307B-9	Sequence 9, Appl
54	210.5	11.8	1091 3 US-08-986-465-5	Sequence 5, Appl
55	208	11.7	868 1 US-08-374-834-1	Sequence 1, Appl
56	207	11.7	868 4 US-08-644-271-1	Sequence 1, Appl
57	207	11.6	434 4 US-09-540-245A-19	Sequence 19, Appl
58	207	11.6	1447 4 US-09-041-886-25	Sequence 25, Appl
59	207	11.6	1447 5 PCT-US94-05277-2	Sequence 2, Appl
60	206	11.6	478 5 PCT-US95-08493-15	Sequence 15, Appl
61	206	11.6	860 5 PCT-US95-08493-11	Sequence 11, Appl
62	206	11.6	868 5 PCT-US95-08493-21	Sequence 21, Appl
63	204	11.5	869 1 US-08-374-834-16	Sequence 16, Appl
64	204	11.5	869 2 US-08-644-271-29	Sequence 29, Appl
65	204	11.5	1501 2 US-08-447-464-3	Sequence 3, Appl
66	204	11.5	1501 2 US-08-716-679-3	Sequence 3, Appl
67	202	11.4	630 2 US-08-752-307B-14	Sequence 14, Appl
68	197.5	11.1	1018 1 US-08-408-093-6	Sequence 6, Appl
69	197.5	11.1	1018 1 US-08-408-420A-6	Sequence 6, Appl
70	197.5	11.1	1018 1 US-08-714-901-6	Sequence 6, Appl
71	197.5	11.1	1018 3 US-08-040-741-6	Sequence 6, Appl
72	197	11.1	1911 1 US-08-348-006B-5	Sequence 5, Appl
73	197	11.1	1911 4 US-08-800-825A-5	Sequence 5, Appl
74	197	11.1	1911 5 PCT-US94-10166-5	Sequence 5, Appl
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77	195.5	11.0	605 2 US-08-752-307B-8	Sequence 8, Appl
78	193.5	10.9	607 2 US-08-752-307B-12	Sequence 12, Appl
79	190.5	10.7	462 2 US-08-752-307B-7	Sequence 7, Appl
80	190.5	10.7	465 2 US-08-752-307B-5	Sequence 5, Appl
81	180	10.1	612 2 US-08-752-307B-11	Sequence 11, Appl
82	166.5	9.4	561 2 US-08-795-868B-14	Sequence 14, Appl
83	164	9.2	596 2 US-08-752-307B-13	Sequence 13, Appl
84	163.5	9.2	287 2 US-08-414-657D-48	Sequence 48, Appl
85	163.5	9.2	304 2 US-08-414-657D-44	Sequence 44, Appl
86	163.5	9.2	304 2 US-08-414-657D-46	Sequence 46, Appl
87	163.5	9.2	325 2 US-08-414-657D-2	Sequence 2, Appl
88	163.5	9.2	325 2 US-08-414-657D-41	Sequence 41, Appl
89	160.5	9.0	287 2 US-08-414-657D-49	Sequence 49, Appl
90	160.5	9.0	310 2 US-08-414-657D-45	Sequence 45, Appl
91	160.5	9.0	315 2 US-08-414-657D-47	Sequence 47, Appl
92	160.5	9.0	338 2 US-08-414-657D-43	Sequence 43, Appl
93	160.5	9.0	338 2 US-08-414-657D-42	Sequence 42, Appl
94	160	9.0	601 2 US-08-795-868B-16	Sequence 16, Appl
95	159.5	9.0	140 3 US-08-986-465-4	Sequence 4, Appl
96	158.5	8.9	340 4 US-09-188-930-184	Sequence 184, App
97	158.5	8.9	1356 2 US-08-810-116-8	Sequence 8, Appl
98	158.5	8.9	1356 2 US-07-930-518A-8	Sequence 8, Appl
99	157	8.8	1356 4 US-09-098-707A-2	Sequence 2, Appl
100	155.5	8.7	338 2 US-08-414-657D-60	Sequence 60, Appl

## ALIGNMENTS

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RESULT 1
US-09-383-586-33
; Sequence 33, Application US/09383586
; Patent No. 6242419
; GENERAL INFORMATION:
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Abernethy, Nevin
; APPLICANT: Kumble, Anand
; APPLICANT: Murison, Greg
; TITLE OF INVENTION: Compounds isolated from stromal cells
; FILE REFERENCE: 11000.1037cl
; CURRENT APPLICATION NUMBER: US/09/383,586
; CURRENT FILING DATE: 1999-08-26
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 33
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Human
US-09-383-586-33

Query Match
Best Local Similarity 100.0%; Score 1779; DB 4; Length 322;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRAPOCCSCRCRCMGSPHPPPEAPQRRRTMSHGRWPAGPHCAAVVEGDPPLTM 60
DB 1 RRAPOCCSCRCRCMGSHRPPPEAPQRRRTMSHGRWPAGPHCAAVVEGDPPLTM 60
QY 61 WTDGRTIHSGMSRFVLPQGLKVKOVERDAGVYCKATNGFSGLSVNTLVLDISP 120
DB 61 WTDGRTIHSGMSRFVLPQGLKVKOVERDAGVYCKATNGFSGLSVNTLVLDISP 120
QY 121 GKESLGPSSSGOEDPASQOMARPRFTOPSKMRRIARPVGSSVRLKCVASGHPRPD 180
DB 121 GKESLGPSSSGOEDPASQOMARPRFTOPSKMRRIARPVGSSVRLKCVASGHPRPD 180
QY 181 TWMKDDQALTRPEAEPKRRKWTLSLKNLRPEDSGKYTCVSNRAGAINATYKVDYIORT 240
DB 181 TWMKDDQALTRPEAEPKRRKWTLSLKNLRPEDSGKYTCVSNRAGAINATYKVDYIORT 240
QY 241 RSKPVLTGTHPVNTYVDFGTTSFQCKVNSDVKPVYIOMLKRVYGAEGRNSTIDVGOK 300
DB 241 RSKPVLTGTHPVNTYVDFGTTSFQCKVNSDVKPVYIOMLKRVYGAEGRNSTIDVGOK 300
QY 301 FVVLPTGDVWSRPDGSYLKPL 322
DB 301 FVVLPTGDVWSRPDGSYLKPL 322

RESULT 2
US-09-383-586-31
; Sequence 31, Application US/09383586
; Patent No. 6242419
; GENERAL INFORMATION:
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Abernethy, Nevin
; APPLICANT: Kumble, Rene
; APPLICANT: Murison, Greg
; TITLE OF INVENTION: Compounds isolated from stromal cells
; FILE REFERENCE: 11000.1037cl
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; CURRENT APPLICATION NUMBER: US/09/383,586
; CURRENT FILING DATE: 1999-08-26
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 31
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Mouse
US-09-383-586-31
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Query Match
Best Local Similarity 77.1%; Score 1371; DB 4; Length 529;
Matches 255; Conservative 8; Mismatches 10; Indels 0; Gaps 0;
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QY 50 PVESDPPPLMTWKDGTTHSGMSRFVLPQGLKVKOVERDAGVYCKATNGFSGLSVN 109
DB 48 PVESDPPPLMTWKDGTTHSGMSRFVLPQGLKVKOVERDAGVYCKATNGFSGLSVN 107
QY 110 YTLVLDISPGEISGPDSSSGOEDPASQOMARPRFTOPSKMRRIARPVGSSVRLK 169
DB 108 YTLVLDISPGEISGPDSSSGOEDPASQOMARPRFTOPSKMRRIARPVGSSVRLK 167
QY 170 CVASGHPRPDITWTKDDQALTRPEAEPKRRKWTLSLKNLRPEDSGKYTCVSNRAGAIN 229
DB 168 CVASGHPRPDITWTKDDQALTRPEAEPKRRKWTLSLKNLRPEDSGKYTCVSNRAGAIN 227
QY 230 ATYKVDYIORTSKPVLTGTHPVNTYVDFGTTSFQCKVNSDVKPVYIOMLKRVYGAEGR 289
DB 228 ATYKVDYIORTSKPVLTGTHPVNTYVDFGTTSFQCKVNSDVKPVYIOMLKRVYGAEGR 287
QY 290 HNSTIDVGOKFVVLPTGDVWSRPDGSYLKPL 322
DB 288 HNSTIDVGOKFVVLPTGDVWSRPDGSYLKPL 320
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RESULT 3
US-09-383-586-32
; Sequence 32, Application US/09383586
; Patent No. 6242419
; GENERAL INFORMATION:
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Abernethy, Nevin
; APPLICANT: Kumble, Rene
; APPLICANT: Murison, Greg
; TITLE OF INVENTION: Compounds isolated from stromal cells
; FILE REFERENCE: 11000.1037cl
; CURRENT APPLICATION NUMBER: US/09/383,586
; CURRENT FILING DATE: 1999-08-26
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 439
; TYPE: PRT
; ORGANISM: Mouse
US-09-383-586-32
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Query Match
Best Local Similarity 57.8%; Score 1029; DB 4; Length 439;
Matches 194; Conservative 4; Mismatches 9; Indels 0; Gaps 0;
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QY 116 DDISPGEISGPDSSSGOEDPASQOMARPRFTOPSKMRRIARPVGSSVRLKCVASGH 175
DB 23 DDISPGEISGPDSSSGOEDPASQOMARPRFTOPSKMRRIARPVGSSVRLKCVASGH 82
QY 176 PRPDITWTKDDQALTRPEAEPKRRKWTLSLKNLRPEDSGKYTCVSNRAGAINATYKVD 235
DB 83 PRPDITWTKDDQALTRPEAEPKRRKWTLSLKNLRPEDSGKYTCVSNRAGAINATYKVD 142
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0y	236	VITRSPKPVLTGHPNVTYVDEGCTSPFOCKVSDVKPVYOMLTKRYEAGEGHNSTID	295
Db	143	VIOTRRSKPVLTGHPNVTYVDEGCTSPFOCKVSDVKPVYOMLTKRYEAGEGHNSTID	202
0y	296	VGGOKFVLPPTGDVWSRPDGSYLKPL	322
Db	203	VGGOKFVLPPTGDVWSRPDGSYLKPL	229
RESULT 4			
US-09-383-630-6			
Sequence 6, Application US/09383630A			
Patent No. 625632			
GENERAL INFORMATION:			
APPLICANT: Avner Yaron et al.			
TITLE OF INVENTION: ANIMAL MODEL FOR FIBROBLAST GROWTH FACTOR RECEPTOR ASSOCIATED CHONDRODYSPLASIA			
NUMBER OF SEQUENCES: 18			
CORRESPONDENCE ADDRESS:			
ADDRESSEE: Mark M. Friedman C/O Anthony Castorina			
STREET: 2001 Jefferson Davis Highway, Suite 207			
CITY: Arlington			
STATE: Virginia			
COUNTRY: United States of America			
ZIP: 22202			
COMPUTER READABLE FORM:			
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk			
COMPUTER: Twinhead* Slimnote-8907x			
OPERATING SYSTEM: MS DOS version 6.2			
SOFTWARE: Word for Windows version 3.11			
to an ASCII file			
CURRENT APPLICATION DATA:			
APPLICATION NUMBER: US/09/383,630A			
FILING DATE: 26-Aug-1993			
CLASSIFICATION: <Unknown>			
PRIOR APPLICATION NUMBER: <Unknown>			
FILING DATE: <Unknown>			
ATTORNEY/AGENT INFORMATION:			
NAME: Friedman, Mark M.			
REGISTRATION NUMBER: 33,893			
REFERENCE/DOCKET NUMBER: 1402/2			
TELECOMMUNICATION INFORMATION:			
TELEPHONE: 972-3-5625553			
TELEFAX: 972-3-5625554			
TELEX: <Unknown>			
INFORMATION FOR SEQ ID NO: 6:			
SEQUENCE CHARACTERISTICS:			
LENGTH: 801			
TYPE: amino acid			
STRANDEDNESS: single			
TOPOLOGY: linear			
SEQUENCE DESCRIPTION: SEQ ID NO: 6:			
US-09-383-630-6			
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Db	6	CVLVFCVAVVAGAGTSEPPGPQQRVYRRAAEYPPGEPSSQGEQVAVGSGDTVLSCHPREGA	65
0y	55	PPPLMTTKDGRITIHSGMSRRFVLPQGLKXKQVEREDAGVYVC--KATNGFSLSVNTL	112
Db	66	PTGPVMAKDGDTGLVAVS--HRTLVGQRLQVLAHSHEDAGVYSCQHRLR---RVLCHEFSV	121
0y	113	VVLDDISFGKSLGPDSSSGQEDPASAQQMARPRFTOPSKMRRRYIARPVSSVRLKCYA	172
Db	122	RVTAPVSSGDEDEDEDVA---EDTGAAYW-----TRPRMDKLLAVPAANTVAFRCFA	172

QY	173	SGHPPEDITWAKDOAL---	RPEAEPRKKKWTISLKNLPEDSGKTYTCVSRNAG	IN	229
Db	173	AGNPPTSPISMLKNGKEFGEHRIGGICIKLRHOOWSLVMSVYPSDRGNATCVAVENKFGSIR			232
QY	230	ATYKVDIOPRKSRCVNLGTHPVNTVDFGGTTSPQCVSRVSRKVIOMLKRVEVGAGGR			289
Db	233	QTYTILVDLERSHHRITLADGLPANOTAILGSDVEFHCKVYSDAOPHIOMLKHEV-----			287
QY	290	HNSTIDVGQKRV-VLPT	306		
Db	288	NGSKVGPDPGTPYVFLKT	305		
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		US-09-383-630-3			
		Sequence 3, Application US/09383630A			
		Patent No. 6265632			
		GENERAL INFORMATION:			
		APPLICANT: Amer Yazon et al.			
		TITLE OF INVENTION: ANIMAL MODEL FOR FIBROBLAST GROWTH			
		FACTOR RECEPTOR ASSOCIATED			
		CHONDRODYSPLASIA			
		NUMBER OF SEQUENCES: 18			
		CORRESPONDENCE ADDRESS:			
		ADDRESSEE: Mark M. Friedman c/o Anthony Castorina			
		STREET: 2001 Jefferson Davis Highway, Suite 207			
		CITY: Arlington			
		STATE: Virginia			
		COUNTRY: United States of America			
		ZIP: 22202			
		COMPUTER READABLE FORM:			
		MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk			
		COMPUTER: Twinhead* Slimnote-890TX			
		OPERATING SYSTEM: MS DOS version 6.2,			
		Windows version 3.11			
		SOFTWARE: Word for Windows version 2.0 converted			
		to an ASCII file			
		CURRENT APPLICATION DATA:			
		APPLICATION NUMBER: US/09/383,630A			
		FILING DATE: 26-Aug-1999			
		CLASSIFICATION: <Unknown>			
		PRIOR APPLICATION DATA:			
		APPLICATION NUMBER: <Unknown>			
		FILING DATE: <Unknown>			
		ATTORNEY/AGENT INFORMATION:			
		NAME: Friedman, Mark M.			
		REGISTRATION NUMBER: 33,883			
		REFERENCE/DOCKET NUMBER: 1402/2			
		TELECOMMUNICATION INFORMATION:			
		TELEPHONE: 972-3-5625553			
		TELEFAX: 972-3-5625554			
		TELEX: <Unknown>			
		INFORMATION FOR SEQ ID NO: 3:			
		SEQUENCE CHARACTERISTICS:			
		LENGTH: 806			
		TYPE: amino acid			
		STRANDEDNESS: single			
		TOPOLOGY: linear			
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		US-09-383-630-3			
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		Best Local Similarity	31.8%	Pred. No. 2.1e-25;	
		Matches	96; Conservative	54; Mismatches	118; Indels 34; Gaps 10;
QY	16	GPSHPPPEPEAQORRTWMSHGRWAGPHCAAVVEGDPP---PL--TMTTKDRTIHS	70		
Db	33	GRAALVPGEPBQDQLVFGSG-----DAVELSCPPIPGGPMGPTVWVKDITGLVP	83		
QY	71	GMSRFVLPQGLKOVEREDAGVYC--KATNGFGSLSVNTTLLVLDLIDISPKESLCPD	128		

Db 84 S-ERVIVGPORLVQVLAHNSHEDSGAYSCRORLTO---RVLCFHSVRYTDAESSGDDEDED 139  
QY 129 SSSGGDEPPASOOWARPRFTOPSKMRRTVIAIPVGSVRLKCVASGHPRPDIWTKDDOA 188  
Db 140 EADDTGVTGAPYW-----TRPERMDKKLLAIPAANTVTRRCRPAAGPTISISLAKGRE 194  
QY 189 LT---RPEAAEPKKKWTLSLKNLRPDSGKYTCRVSNRAGAINATYKVDTIQRTRSKPV 245  
Db 195 FRGEHRIGGJIKLRHQOQSLVMSVPSDRGNNTCYVENKRGSIROTYYTLDLVLEERSPHRPI 254  
QY 246 LCTHPVNTVDFGGTTSPOCKYRSDVKPYIOWLKRYEGAGEGHNSTIDVGCKFY-VL 304  
Db 255 LQGLLANQVAVGSDVEYFCKVYSDAQPHIOWLKHEV-----NGSKVGPDTGPTVTVL 309  
QY 305 PT 306  
Db 310 KT 311

RESULT 6  
US-08-471-570-14  
Sequence 14, Application US/08471570  
Patent No. 5750371  
GENERAL INFORMATION:  
APPLICANT: IGARASHI, Koichi  
APPLICANT: SEMOO, Masaharu  
APPLICANT: WATANABE, Tatsuya  
TITLE OF INVENTION: PROTEIN, DNA AND USE THEREOF  
NUMBER OF SEQUENCES: 18  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &  
STREET: 130 Water Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: US  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/471,570  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/149,664  
FILING DATE:  
APPLICATION NUMBER: US 07/743369  
FILING DATE: 16-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: LINEK, Ernest V  
REGISTRATION NUMBER: 29822  
REFERENCE/DOCKET NUMBER: 40897  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)523-3400  
TELEFAX: (617)523-6440  
TELEX: 200291 STRE UR  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 355 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-471-570-14

Query Match 21.1%; Score 375.5; DB 1; Length 355;  
Best Local Similarity 29.9%; Pred. No. 1,1e-25;  
Matches 97; Conservative 55; Mismatches 129; Indels 43; Gaps 10;

QY 23 PPEAQRMTIRSHGHWAGPICAANVPYEG-----DPPPLIMWTKDGRTIHSGWSRF 75

Db 15 PEEPTKYQI-----SQPEYVVAAPGESLEVRCLLKDAAYISWTKDG--VHLGPNNR 64  
QY 76 RVL-PQGLAKVOYREDAGYVVCATNGFSGLSYNTLVLDISPCKESLGPDSGGQ 134  
Db 65 TLIGEVYLQIKGATPPRDSGLYACTASRTVSEWYFVWNTDAISSGD-----EDDTGDA 120  
QY 135 EDPASQ---QWAPRFPQPSKMRRTVIAIPVGSVRLKCVASGHPRPDIWTKDDOALT- 190  
Db 121 EDVYSESNKRAPIYWTNTEKMEKRLHVAIPAANTVTRCPCAGNPMTMRMLKNGEFGQ 180  
QY 191 --RPEAAEPKKKWTLSLKNLRPDSGKYTCRVSNRAGAINATYKVDTIQRTRSKPVLTG 248  
Db 181 EHRIGGYKRVANQHSLSLMSVPSDKGNTCYVENEGSINHYYHLDLVLEERSPHRPIQA 240  
QY 249 THPVNTVDFGGTTSPOCKYRSDVKPYIOWLKRYE-----YAGS-----RHNSTIDV 296  
Db 241 GLPANNASTVVGSDVEYFCKVYSDAQPHIOWIKHVEKNGSGYGDGLPYLKLKHSQ---I 297  
QY 297 GGOKFVVLPTGDVWSRPDGSYLNK 320  
Db 298 NSSNAEVLALFNVTEDAGEYICK 321

RESULT 7  
US-08-471-570-6  
Sequence 6, Application US/08471570  
Patent No. 5750371  
GENERAL INFORMATION:  
APPLICANT: IGARASHI, Koichi  
APPLICANT: SEMOO, Masaharu  
APPLICANT: WATANABE, Tatsuya  
TITLE OF INVENTION: PROTEIN, DNA AND USE THEREOF  
NUMBER OF SEQUENCES: 18  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &  
STREET: 130 Water Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: US  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/471,570  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/149,664  
FILING DATE:  
APPLICATION NUMBER: US 07/743369  
FILING DATE: 16-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: LINEK, Ernest V  
REGISTRATION NUMBER: 29822  
REFERENCE/DOCKET NUMBER: 40897  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)523-3400  
TELEFAX: (617)523-6440  
TELEX: 200291 STRE UR  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 643 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-471-570-6



TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-07-640-029-1

Query Match 21.0%; Score 373; DB 1; Length 816;  
Best Local Similarity 30.1%; Pred. No. 5,9e-25;

Matches 89; Conservative 46; Mismatches 115; Indels 46; Gaps 8;

QY 20 RPP-PEAQRKRTKSHGMPAGHCAAVPYEG-----DPPILTMW 61  
DB 22 RPSSTLEQAPW-----GAPVEVESFLVHPGDLQLRCLRDVQGINW 66  
QY 62 TKDRTIHSGRPRVLPOGLKVOVEREDAGVYCATNGFSLVNTLVLDISP 121  
DB 67 LRDOVLAES-NRTRIGEVEVDSPADSGIACYTSSSGS-DTTTISVNSDALPS 124  
QY 122 KESIGPDSGGOE-----DPAQOVARPRFTOPSKMRRIARPVGSVRLKCVASGH 175  
DB 125 SEDDDDDSSSEKKEKETDNTKPNVPAPYWTSPKEMKKLHAPAAKTVKFCPSGT 184  
QY 176 PRDITMKDQALTRP-----AAEPKKWTLSLKNLRPDSGKTYCRVSNRAGAINAT 231  
DB 185 NPLTLRLKNGKEF-KPDHIGYKRYATWSTIIMDSVPSDKGNTYCIENEGSINTHT 243  
QY 232 YKVDVORTSKPYLTGTHPNTTVDGCTTSPQCKVRSVPKPYIOMLKRREYGA 287  
DB 244 YQDVVERSHRPILOGLPANKTVLALGSNVEFMCKYSDPQPHIQMLKHEMGSK 299

RESULT 10  
US-08-451-822A-13  
Sequence 13, Application US/08451822A  
Patent No. 5863888

## GENERAL INFORMATION:

APPLICANT: Dione, Craig A  
APPLICANT: Crumley, Greg  
APPLICANT: Jaye, Michael C  
APPLICANT: Schlessinger, Joseph  
TITLE OF INVENTION: Fibroblast Growth Factor Receptors  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Rhone-Poulenc Rorer Legal Department  
STREET: 500 Arcola Road  
CITY: Collegeville  
STATE: PA  
COUNTRY: USA  
ZIP: 19426

## COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/451,822A  
FILING DATE: 26-MAY-1995  
CLASSIFICATION: 435

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/323,430  
FILING DATE: 14-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/934,372  
FILING DATE: 21-AUG-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/549,587  
FILING DATE: 06-JUL-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Savitzky, Martin

REGISTRATION NUMBER: 29,699  
REFERENCE/DOCKET NUMBER: A0496E  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (610) 454-3816  
TELEFAX: (610) 454-3808

## INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:

LENGTH: 821 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-451-822A-13

Query Match 20.9%; Score 371.5; DB 2; Length 821;  
Best Local Similarity 31.6%; Pred. No. 8.1e-25;

Matches 90; Conservative 50; Mismatches 112; Indels 33; Gaps 8;

QY 23 PPEAQRKRTKSHGMPAGHCAAVPYEG-----DPPILTMKDGRTIHSGRPR 75  
DB 35 PEEPRTKYQI-----SQPEYVAAPGSLERVLCLKDAVAISWTKDG-VHLAPNNR 84  
QY 76 RVL-POGLKVOVEREDAGVYCATNGFSLVNTLVLDISPRESLGPDSGGQ 134  
DB 85 TVLIGETLQKATPRDQGLACTASRYVSETWYFVNTVTDALSSGD---EDDTDA 140  
QY 135 EDPASQ---OWANPRFTOPSKMRRIARPVGSVRLKCVASGHPRPDITMKDQALTR 190  
DB 141 EDFVSESNKRAPYWTNTEKMEKKLHAPAAANTVAFRCAGAGNPMPTRLKNGKEFKQ 200  
QY 191 --RPEAEPKKKWTLSLKNLRPDSGKTYCRVSNRAGAINATYKVDVORTSKPYLTG 248  
DB 201 EHRIGYKRYNOMHSLIMSVPDSKGYTCVYENEGSINTHTYHLDVVERSHRPILOA 260  
QY 249 THPNTTVDGCTTSPQCKVRSVPKPYIOMLKRVE-----YGAEG 288  
DB 261 GLPANSYVGGVVERCKYSDPQPHIQMLKHEMGSKYGDG 305

RESULT 11  
US-07-921-807B-3  
Sequence 3, Application US/07921807B  
Patent No. 5474914

## GENERAL INFORMATION:

APPLICANT: SPAETE, RICHARD  
TITLE OF INVENTION: METHOD OF INCREASING EXPRESSION  
TITLE OF INVENTION: OF VIRAL PROTEINS  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSER: CHIRON CORPORATION  
STREET: 4560 Horton Street - R440  
CITY: Emeryville  
STATE: CA  
COUNTRY: USA  
ZIP: 94608-2916

## COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/921,807B  
FILING DATE: 29-SEP-1992  
CLASSIFICATION: 435

## ATTORNEY/AGENT INFORMATION:

NAME: MCCLUNG, BARBARA G.  
REGISTRATION NUMBER: 33,113  
REFERENCE/DOCKET NUMBER: 0209.001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (510) 601-2708  
TELEFAX: (510) 655-3542

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:  
LENGTH: 820 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear

MOLECULE TYPE: protein  
US-07-921-807B-3

Query Match 20.5%; Score 364.5; DB 1; Length 820;  
Best Local Similarity 30.4%; Pred. No. 3,4e-24;  
Matches 88; Conservative 43; Mismatches 115; Indels 43; Gaps 8;

QY 20 RPP--PEAQRWRTKSHGMRGPHCAAVPEG-----DPPPLTW 61  
DB 22 RSPFTLEQAQW-----GAVEVESFLVHGDLLQRLCRDRDVGSI 66  
QY 62 TKDGRTHSGMSRFRVLPGGLKQVERDAGYVVCATNGFSLSVNTLVLDISPG 121  
DB 67 LRDSVQLAES-NRRITGEEVEVDSPADSGIACVTSFSGS-DITYFSVNSDALPS 124  
QY 122 KESLGPSSSGGQF---DPAQOMARRFTQPSKMRRIARVPVSSVRLKCVASGHRP 178  
DB 125 SEDDDDDSSSEKEKENDTRPNVAPYWTSPKMKKKLAHVPAKTYKFCPSGTPNP 184  
QY 179 DITMKDDQALTRPE---AAEPKKKWTLSLKNLRPDSGKYTCRVSNRAGAINATYKV 234  
DB 185 TLRLKNGKER-KPDHRIGGKVRATWSTIMDSVPSDKGNTYCIYENEGSINHYYQL 243  
QY 235 DVIGTRSKPVLGTHTPVNTTDFGTTSPQCKYRSDVKPYIQLKRYE 283  
DB 244 DVERSPHRPILOGLPANKTVLGSNVEFMCKYSDPQPHIQLKHIE 292

## RESULT 12

US-08-441-944A-3  
Sequence 3, Application US/08441944A  
Patent No. 5767250  
GENERAL INFORMATION:  
APPLICANT: SPAETE, RICHARD  
TITLE OF INVENTION: METHOD OF INCREASING EXPRESSION  
TITLE OF INVENTION: OF VIRAL PROTEINS  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CHIRON CORPORATION  
STREET: 4560 Horton Street - R440  
CITY: Emeryville  
STATE: CA  
COUNTRY: USA  
ZIP: 94608-2916  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/441,944A  
FILING DATE: 16-MAY-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/921,807  
FILING DATE: 29-SEP-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: MCCLUNG, BARBARA G.  
REGISTRATION NUMBER: 33,113  
REFERENCE/DOCKET NUMBER: 0209.001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (510) 601-2708  
TELEFAX: (510) 655-3542  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 820 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-441-944A-3

Query Match 20.5%; Score 364.5; DB 1; Length 820;  
Best Local Similarity 30.4%; Pred. No. 3,4e-24;  
Matches 88; Conservative 43; Mismatches 115; Indels 43; Gaps 8;

QY 20 RPP--PEAQRWRTKSHGMRGPHCAAVPEG-----DPPPLTW 61  
DB 22 RSPFTLEQAQW-----GAVEVESFLVHGDLLQRLCRDRDVGSI 66  
QY 62 TKDGRTHSGMSRFRVLPGGLKQVERDAGYVVCATNGFSLSVNTLVLDISPG 121  
DB 67 LRDSVQLAES-NRRITGEEVEVDSPADSGIACVTSFSGS-DITYFSVNSDALPS 124  
QY 122 KESLGPSSSGGQF---DPAQOMARRFTQPSKMRRIARVPVSSVRLKCVASGHRP 178  
DB 125 SEDDDDDSSSEKEKENDTRPNVAPYWTSPKMKKKLAHVPAKTYKFCPSGTPNP 184  
QY 179 DITMKDDQALTRPE---AAEPKKKWTLSLKNLRPDSGKYTCRVSNRAGAINATYKV 234  
DB 185 TLRLKNGKER-KPDHRIGGKVRATWSTIMDSVPSDKGNTYCIYENEGSINHYYQL 243  
QY 235 DVIGTRSKPVLGTHTPVNTTDFGTTSPQCKYRSDVKPYIQLKRYE 283  
DB 244 DVERSPHRPILOGLPANKTVLGSNVEFMCKYSDPQPHIQLKHIE 292

## RESULT 13

US-08-439-992A-1  
Sequence 1, Application US/08439992A  
Patent No. 625454  
GENERAL INFORMATION:  
APPLICANT: Kiefer, Michael C.  
APPLICANT: Pablo, Valenzuela D.T.  
TITLE OF INVENTION: Expression and Use of Human Fibroblast  
TITLE OF INVENTION: Receptor  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Chiron Corporation  
STREET: 4560 Horton Street  
CITY: Emeryville  
STATE: CA  
COUNTRY: USA  
ZIP: 94608  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/439,992A  
FILING DATE: 12-MAY-1995  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Chung, Ling-Fong  
REGISTRATION NUMBER: 36,482  
REFERENCE/DOCKET NUMBER: 0165.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 510-923-2704  
TELEFAX: (510) 655-3542  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 820 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-439-992A-1

Query Match 20.5%; Score 364.5; DB 4; Length 820;  
Best Local Similarity 30.4%; Pred. No. 3,4e-24;  
Matches 88; Conservative 43; Mismatches 115; Indels 43; Gaps 8;

```

PCT-US93-05703-2
? Sequence 2, Application PC/TUS9305703
? GENERAL INFORMATION:
? APPLICANT: Nova, Michael P.
? APPLICANT: Gonzalez, Ana-Maria
? APPLICANT: Baird, J. Andrew
? TITLE OF INVENTION: Process for Detection of Neoplasia
? TITLE OF INVENTION: Disease
? NUMBER OF SEQUENCES: 2
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Fitch, Even, Tabin & Flannery
? STREET: 135 South LaSalle Street, Suite 900
? CITY: Chicago
? STATE: IL
? COUNTRY: USA
? ZIP: 60603
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: PCT/US93/05703
? FILING DATE: 19930614
? CLASSIFICATION:
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 07/900,646
? FILING DATE: 18-JUN-1992
? ATTORNEY/AGENT INFORMATION:
? NAME: Seidman, Stephanie
? REGISTRATION NUMBER: 33,779
? REFERENCE/DOCKET NUMBER: 54625PCT
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 619-552-1311
? TELEFAX: 619-552-0095
? INFORMATION FOR SEQ ID NO: 2:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 351 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: unknown
? MOLECULE TYPE: protein
? FEATURE:
? NAME/KEY: Protein
? LOCATION: 1..351
? OTHER INFORMATION:
? PCT-US93-05703-2 /note="Sequence of
? extracellular domain of an FGFRI"

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1      RESULT 15
2      US-07-640-029-2
3      ; Sequence 2, Application US/07640029
4      ; Patent No. 5229501
5      ;
6      ; GENERAL INFORMATION:
7      ; APPLICANT: Kiefer, Michael C.
8      ; APPLICANT: Valenzuela, Pablo D.T.
9      ; APPLICANT: Barr, Philip J.
10     ; TITLE OF INVENTION: Expression and Use of Human Fibroblast
11     ; TITLE OF INVENTION: Growth Factor Receptor
12     ; NUMBER OF SEQUENCES: 12
13     ; CORRESPONDENCE ADDRESSES:
14     ; ADDRESS: Chiron Corporation
15     ; STREET: 4560 Horton Street
16     ; CITY: Emeryville
17     ; STATE: California
18     ; COUNTRY: USA
19     ; ZIP: 94608
20     ;
21     ; COMPUTER READABLE FORM:
22     ; MEDIUM TYPE: Floppy disk
23     ; COMPUTER: IBM PC compatible
24     ; OPERATING SYSTEM: PC-DOS/MS-DOS
25     ; SOFTWARE: Patent In Release #1.0, Version #1.25
26     ; CURRENT APPLICATION DATA:
27     ; APPLICATION NUMBER: US/07/640,029
28     ; FILING DATE: 19910111
29     ; CLASSIFICATION: 530
30     ;
31     ; ATTORNEY/AGENT INFORMATION:
32     ; NAME: McClung, Barbara G.
33     ; REGISTRATION NUMBER: 33,113
34     ; REFERENCE/DOCKET NUMBER: CH-165
35     ; TELECOMMUNICATION INFORMATION:
36     ; TELEPHONE: 510-601-2708
37     ; TELEFAX: 510-655-3542
38     ;
39     ; INFORMATION FOR SEQ ID NO: 2:
40     ; SEQUENCE CHARACTERISTICS:
41     ; LENGTH: 817 amino acids
42     ; TYPE: AMINO ACID
43     ; STRANDEDNESS: single
44     ; TOPOLOGY: linear
45     ;
46     ; MOLECULE TYPE: peptide
47     ;
48     ; US-07-640-029-2

```

Query Match	20.38;	Score 360.5;	DB 1;	Length 817;
Best Local Similarity	29.98;	Pred. No. 7.6e-24;		
Matches 87;	Conservative 45;	Mismatches 114;	Indels 45;	Gaps 8





Db 125 SEDDDDDDSSSEKETDNTKPNMPPVAPWTSEKMEKKLHNAVPAKTYKFKCPSSGTP 184  
QY 177 RPDITWKKDDOALTRPE----AAEPKKKWTLSLKNLRPDSGKYTCRVSNRAGAINATY 232  
Db 185 NPTLRMLKKNKEF-KPDHRIGYKVRATWSIIMDSVPSDKGNVTCIVENEGYSINHYY 243  
QY 233 KVDVIOQTRSKPVLGTGHPVNTVDFGTTSFQCKVRSQVDPKPYIOWMLKRYE 283  
Db 244 QLDVERSHPRPILOAGLPANKTVALGNSVNEFCKYISDPQPHIOWMLKHIE 294

## RESULT 18

US-08-441-944A-4  
; Sequence 4, Application US/08441944A  
; Patent No. 5767250  
; GENERAL INFORMATION:  
; APPLICANT: SPAETE, RICHARD  
; TITLE OF INVENTION: METHOD OF INCREASING EXPRESSION  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CHIRON CORPORATION  
; STREET: 4560 Horton Street - R440  
; CITY: Emeryville  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94608-2916  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/441,944A  
; FILING DATE: 16-MAY-1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/921,807  
; FILING DATE: 29-SEP-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MCCLUNG, BARBARA G.  
; REGISTRATION NUMBER: 33,113  
; REFERENCE/DOCKET NUMBER: 0209,001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (510) 601-2708  
; TELEFAX: (510) 655-3542  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 822 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-441-944A-4

Query Match 20.3%; Score 360.5; DB 1; Length 822;  
Best Local Similarity 29.9%; Pred. No. 7.7e-24;  
Matches 87; Conservative 45; Mismatches 114; Indels 45; Gaps 8;

QY 20 RPP--PEAPQWRTRMSHGRMPAGPHCAAAVVEG-----DPPPLTMW 61  
Db 22 RSPPLPEQAQFW-----GAPVEVESFLVHPGDLQLRCRLRBDVQSIWM 66  
QY 62 TDDGRTIHSGMRFVLPQGLKVKOVERDAGVYVCATNGSGLSVNTLVLDISPG 121  
Db 67 LRDGVQLAES-NKRTITGEVEVDSPADSGLIACVTSPPSGS-DTTYFSVNSDALPS 124  
QY 122 KSLSLPDSSSGGQEDPA-----SQQWARPRTQPSKMRRTVARIAPVSSVRLKCVASGHP 176  
Db 125 SDDDDDDSSSEKETDNTKPNRMPVAPYWTSEKMEKKLHNAVPAKTYKFKCPSSGTP 184

QY 177 RPDITWKKDDOALTRPE----AAEPKKKWTLSLKNLRPDSGKYTCRVSNRAGAINATY 232  
Db 185 NPTLRMLKKNKEF-KPDHRIGYKVRATWSIIMDSVPSDKGNVTCIVENEGYSINHYY 243  
QY 233 KVDVIOQTRSKPVLGTGHPVNTVDFGTTSFQCKVRSQVDPKPYIOWMLKRYE 283  
Db 244 QLDVERSHPRPILOAGLPANKTVALGNSVNEFCKYISDPQPHIOWMLKHIE 294

## RESULT 19

US-08-451-822A-12  
; Sequence 12, Application US/08451822A  
; Patent No. 5863888  
; GENERAL INFORMATION:  
; APPLICANT: Dionne, Craig A  
; APPLICANT: Crumley, Greg  
; APPLICANT: Jaye, Michael C  
; APPLICANT: Schlessinger, Joseph  
; TITLE OF INVENTION: Fibroblast Growth Factor Receptors  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Rhone-Poulenc Rorer Legal Department  
; STREET: 500 Atcola Road  
; CITY: Collegeville  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19426  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/451,822A  
; FILING DATE: 26-MAY-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/323,430  
; FILING DATE: 14-OCT-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/934,372  
; FILING DATE: 21-AUG-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/549,587  
; FILING DATE: 06-JUL-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Savitzky, Martin  
; REGISTRATION NUMBER: 29,699  
; REFERENCE/DOCKET NUMBER: A0496E  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (610) 454-3816  
; TELEFAX: (610) 454-3808  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 822 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-451-822A-12

Query Match 20.3%; Score 360.5; DB 2; Length 822;  
Best Local Similarity 29.9%; Pred. No. 7.7e-24;  
Matches 87; Conservative 45; Mismatches 114; Indels 45; Gaps 8;

QY 20 RPP--PEAPQWRTRMSHGRMPAGPHCAAAVVEG-----DPPPLTMW 61  
Db 22 RSPPLPEQAQFW-----GAPVEVESFLVHPGDLQLRCRLRBDVQSIWM 66  
QY 62 TDDGRTIHSGMRFVLPQGLKVKOVERDAGVYVCATNGSGLSVNTLVLDISPG 121  
Db 67 LRDGVQLAES-NKRTITGEVEVDSPADSGLIACVTSPPSGS-DTTYFSVNSDALPS 124



Db 125 SEDDDDDSSSEKETDNTKPNRPVAPYWTSPKMEKTLHAVPAKTVKFCPSGCT 184  
QY 177 RPDITWMDKDALTRPE---AAEPKKKWTLISKLNPEDSGKTCVRNAGAINFY 232  
Db 185 NPTLRMLKNGKEF-KPDHIGIKYKRYATWSIIMDSVSPSKGNTTCIENEGSINHTY 243  
QY 233 KVDVIQRTSRKPVLTGTHPVNTTVDGTTSFQCKVRSDDVAPVIOMLKRV 283  
Db 244 QLDVVERSPHRILOAGLPANKTVALGNSVEFMCKVSDPQPHIQMLKHIE 294

## RESULT 22

US-09-383-586-30  
; Sequence 30, Application US/09383586  
; Patent No. 6242419  
; GENERAL INFORMATION:  
; APPLICANT: Strachan, Lorna  
; APPLICANT: Sleeman, Matthew  
; APPLICANT: Abernethy, Nevin  
; APPLICANT: Onrust, Rene  
; APPLICANT: Kumble, Anand  
; APPLICANT: Murison, Greg  
TITLE OF INVENTION: Compounds isolated from stromal cells  
TITLE OF INVENTION: and methods for their use  
FILE REFERENCE: 11000.1037c1  
CURRENT APPLICATION NUMBER: US/09/383.586  
CURRENT FILING DATE: 1999-08-26  
NUMBER OF SEQ ID NOS: 38  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 30  
LENGTH: 126  
TYPE: PRT  
ORGANISM: Mouse  
FEATURE:  
NAME/KEY: UNSURE  
LOCATION: (123)...(123)  
US-09-383-586-30

Query Match 19.7%; Score 350; DB 4; Length 126;  
Best Local Similarity 97.0%; Pred. No. 5.3e-24;  
Matches 65; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 256 VDRGGTTSFQCKVRSDDVAPVIOMLKRVYGAEGRHNSTIDVGCGKTVLPTGDWMSRPDG 315  
Db 1 VDRGGTTSFQCKVRSDDVAPVIOMLKRVYGEGRHNSTIDVGCGKTVLPTGDWMSRPDG 60  
QY 316 SYLNKPL 322  
Db 61 SYLNKLL 67

## RESULT 23

US-08-166-717D-6  
; Sequence 6, Application US/08166717D  
; Patent No. 5789182  
; GENERAL INFORMATION:  
; APPLICANT: Yayon, Avner  
; APPLICANT: Ornitz, David M.  
; APPLICANT: Klagsbrun, Michael  
; APPLICANT: Ledger, Philip  
TITLE OF INVENTION: SYSTEM FOR ASSAYING BINDING  
TITLE OF INVENTION: TO A HEPARIN-BINDING GROWTH  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Clark & Elbing LLP  
STREET: 176 Federal Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02110  
COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 MB  
COMPUTER: IBM COMPATIBLE  
OPERATING SYSTEM: WINDOWS 95  
SOFTWARE: WordPerfect (Version 7.0)  
CURRENT APPLICATION NUMBER: US/08/166,717D  
FILING DATE: 12/14/93  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/631,717  
FILING DATE: 12/20/90  
ATTORNEY/AGENT INFORMATION:  
NAME: Kristina Bieker-Brady  
REGISTRATION NUMBER: 39,109  
REFERENCE/DOCKET NUMBER: 00383/017002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 723-4123  
TELEFAX: (617) 723-8962  
TELEX:  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 820  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-166-717D-6

Query Match 19.6%; Score 349.5; DB 1; Length 820;  
Best Local Similarity 30.5%; Pred. No. 7.3e-23;  
Matches 89; Conservative 42; Mismatches 112; Indels 49; Gaps 10;

QY 20 RPPF--PEAPORMTKRSRWRPAGPCAAVPE-----GDPPPLM----- 60  
Db 22 RPAFLPEQAQPW-----GPEVESLVLVHPEDDLQLCRLRDVQST 64  
QY 61 -WTKDG-RTIHSGWSRREVLPOGLKQVEREDAGVYVCKATNGFSLSYNTLVVLDI 118  
Db 65 NWXXDGVQVLES--NRRIRIGEVEVDSIPADSGLACTSSPSGS-DITYSVANSDA 121  
QY 119 SPKESLSGPPSSGGGE--DPAQOMARPRFTOPSKMRRRYIARPYGSSVRLKCAVSGH 175  
Db 122 LPSEDDDDHDSSEKETDNTKPNRPVAPYWTSPKMEKTLHRVPAKTVKFCPSGCT 181  
QY 176 RPDITWMDKDALTRPE---AAEPKKKWTLISKLNPEDSGKTCVRNAGAINAT 231  
Db 182 NPTLRMLKNGKEF-KPDHIGIKYKRYATWSIIMDSVSPSKGNTTCIENEGSINHT 240  
QY 232 YKVDVIQRTSRKPVLTGTHPVNTTVDGTTSFQCKVRSDDVAPVIOMLKRV 283  
Db 241 QLDVVERSPHRILOAGLPANKTVALGNSVEFMCKVSDPQPHIQMLKHIE 292

## RESULT 24

US-07-640-029-5  
; Sequence 5, Application US/07640029  
; Patent No. 5229501  
; GENERAL INFORMATION:  
; APPLICANT: Kiefer, Michael C.  
; APPLICANT: Valenzuela, Pablo D.T.  
; APPLICANT: Barr, Philip J.  
TITLE OF INVENTION: Expression and Use of Human Fibroblast  
TITLE OF INVENTION: Growth Factor Receptor  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Chiron Corporation  
STREET: 4560 Horton Street  
CITY: Emeryville  
STATE: California  
COUNTRY: USA  
ZIP: 94608  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/640,029  
FILING DATE: 19910111  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: McClung, Barbara G.  
REGISTRATION NUMBER: 33,113  
REFERENCE/DOCKET NUMBER: CH-165  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 510-601-2708  
TELEFAX: 510-655-3542  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 300 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-07-640-029-5

Query Match 17.3%; Score 308; DB 1; Length 300;  
Best Local Similarity 35.6%, Pred. No. 9.2e-20;  
Matches 62; Conservative 30; Mismatches 74; Indels 8; Gaps 3;  
QY 117 DISPKESLGPSSSGGQ---DPASQOARPRFTOPSKMRRTIARPVGSSVRLKCVAS 173  
DB 31 DALPSEDDDDDDSSSEKETDNTPVPVAPYWTSPKMEKTLHAVPAKTVKFCPS 90  
QY 174 GHPREDITWKKDDQALTRPE---AAEPKRRKWTLSLKNLPEDSGKTYTCRYSNRAGALN 229  
DB 91 GTPNPTLWLNKNGKEF-KPDHRIGYKVRYATWSLIMDSVPSDKGNTTCIVENEYGSIN 149  
QY 230 ATYKVDVIQRTSRKPVLTGTHPVNTTVDFGGTTSFQCKVRSQVVKPVYIOMLKRE 283  
DB 150 HTYQLDVVERSPHRILOAGLPANKTVALGSNVEFMCKVYSDPOPHIOMLKHI 203

RESULT 25  
US-08-439-992A-5  
Sequence 5, Application US/08439992A  
Patent No. 6255454  
GENERAL INFORMATION:  
APPLICANT: Kiefer, Michael C.  
APPLICANT: Pablo, Valenzuela D.T.  
APPLICANT: Philip, Barr J.  
TITLE OF INVENTION: Expression and Use of Human Fibroblast  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Chiron Corporation  
STREET: 4560 Horton Street  
CITY: Emeryville  
STATE: CA  
COUNTRY: USA  
ZIP: 94608  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/439,992A  
FILING DATE: 12-MAY-1995  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Chung, Ling-fong  
REGISTRATION NUMBER: 36,482  
REFERENCE/DOCKET NUMBER: 0165, 004  
TELECOMMUNICATION INFORMATION:

TELEPHONE: 510-923-2704  
TELEFAX: (510) 655-3542  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 300 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-439-992A-5

Query Match 17.3%; Score 308; DB 4; Length 300;  
Best Local Similarity 35.6%, Pred. No. 9.2e-20;  
Matches 62; Conservative 30; Mismatches 74; Indels 8; Gaps 3;  
QY 117 DISPKESLGPSSSGGQ---DPASQOARPRFTOPSKMRRTIARPVGSSVRLKCVAS 173  
DB 31 DALPSEDDDDDDSSSEKETDNTPVPVAPYWTSPKMEKTLHAVPAKTVKFCPS 90  
QY 174 GHPREDITWKKDDQALTRPE---AAEPKRRKWTLSLKNLPEDSGKTYTCRYSNRAGALN 229  
DB 91 GTPNPTLWLNKNGKEF-KPDHRIGYKVRYATWSLIMDSVPSDKGNTTCIVENEYGSIN 149  
QY 230 ATYKVDVIQRTSRKPVLTGTHPVNTTVDFGGTTSFQCKVRSQVVKPVYIOMLKRE 283  
DB 150 HTYQLDVVERSPHRILOAGLPANKTVALGSNVEFMCKVYSDPOPHIOMLKHI 203

Search completed: May 2, 2002, 08:50:20  
Job time: 122 sec





93 221.5 12.5 729 5 Q9VED5 O9ved5 drosophila  
 94 220 12.4 1344 11 Q9Z2I4 O9z2i4 mus musculus  
 95 219.5 12.3 555 4 Q9U0H8 Q9ugh8 homo sapien  
 96 219 12.3 2174 5 Q9GCR0 Q9gcr0 drosophila  
 97 218.5 12.3 1033 5 Q9V643 Q9v643 drosophila  
 98 218.5 12.3 6642 5 O01761 O01761 caenorhabdi  
 99 216.5 12.2 163 13 Q934I8 Q934i8 gallus gall  
 100 215.5 12.1 554 4 Q9UQH9 Q9ugh9 homo sapien

## ALIGNMENTS

RESULT 1  
 Q9BXN7 PRELIMINARY; PRT; 497 AA.  
 AC Q9BXN7;  
 DT 01-JUN-2001 (Tremblrel. 17, Created)  
 DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)  
 DE FGF HOMOLOGOUS FACTOR RECEPTOR.  
 GN FHR.  
 OS Homo sapiens (Human).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 NX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Aggarwal S., Xie M.-H., Foster J., Frantz G., Stinson J., Corpuz R.T.,  
 RA Simmons L., Hillan K., Yansura D.G., Vandlen R.L., Goddard A.D.,  
 RA Gurney A.L.;  
 RT "FHR, a novel fibroblast growth factor receptor that uniquely binds  
 RT the fibroblast growth factor homologous factors";  
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF312678; AAK15273.1;  
 KW Receptor.  
 SQ SEQUENCE 497 AA; 53757 MW; 57301F4F36357360 CRC64;

## Query Match

Best Local Similarity 81.4%; Score 1448; DB 4; Length 497;  
 Matches 272; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 50 PVEGDPPPLTMTKDGRTIHSGMSRFVLPQGLKVKOVEREDAGVYCKATNGFGLSVN 109  
 |||||||  
 DB 52 PVEGDPPPLTMTKDGRTIHSGMSRFVLPQGLKVKOVEREDAGVYCKATNGFGLSVN 111  
 |||||||  
 QY 110 YTLVVLDDISPGRKSLGPDSSSGQEDPASQOMARPRFTQPSKMRRVIAAPVGSVRLK 169  
 |||||||  
 DB 112 YTLVVLDDISPGRKSLGPDSSSGQEDPASQOMARPRFTQPSKMRRVIAAPVGSVRLK 171  
 |||||||  
 QY 170 CVASGHRPDIITMMKDDQALTRPEAAEPRKKKWTLSLKNRPEDSGKYTCRVSNRAGAIN 229  
 |||||||  
 DB 172 CVASGHRPDIITMMKDDQALTRPEAAEPRKKKWTLSLKNRPEDSGKYTCRVSNRAGAIN 231  
 |||||||  
 QY 230 ATYKVDVIOIRTSKRPVLTGHPVNTVDFGTTSFQCKVRSVDKPYIOWMLKREYGAEGR 289  
 |||||||  
 DB 232 ATYKVDVIOIRTSKRPVLTGHPVNTVDFGTTSFQCKVRSVDKPYIOWMLKREYGAEGR 291  
 |||||||  
 QY 290 HNSTIDVGOKFYVLPFGDWSRPDGSYLKPL 322  
 |||||||  
 DB 292 HNSTIDVGOKFYVLPFGDWSRPDGSYLKPL 324  
 |||||||

RESULT 2  
 Q9H4D7 PRELIMINARY; PRT; 504 AA.  
 AC Q9H4D7;  
 DT 01-MAR-2001 (Tremblrel. 16, Created)  
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)  
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)  
 DE FGFRL-LIKE PROTEIN PRECURSOR (FIBROBLAST GROWTH FACTOR RECEPTOR 5).  
 GN FGFRL OR FGFRL.

OS Homo sapiens (Human).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 NX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-CARTILAGE;  
 RX PubMed-11031111;  
 RA Wiedemann M., Trub B.;  
 RT "Characterization of a novel protein (FGFRL1) from human cartilage  
 RT related to FGF receptors.";  
 RL Genomics 69: 275-279 (2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-2167383; PubMed-11267671;  
 RA Kim I., Moon S.O., Yu K.H., Kim U.H., Koh G.Y.;  
 RT "A novel fibroblast growth factor receptor-5 preferentially expressed  
 RT in the pancreas.";  
 RL Biochim. Biophys. Acta 1518:152-156(2001).  
 CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX  
 CC DOMAIN.  
 DR EMBL: AJ277437; CAC14171.1;  
 DR EMBL: AF279689; AAK26742.1;  
 DR Interpro: IPR003599; Ig.  
 DR Interpro: IPR003598; Ig\_C2.  
 DR Interpro: IPR003600; Ig\_Like.  
 DR Interpro: IPR003006; Ig\_MHC.  
 DR Pfam: PF00047; Ig\_3.  
 DR SMART: SM00409; Ig\_3.  
 DR SMART: SM00408; IgC2\_3.  
 DR SMART: SM00410; Ig\_Like; 2.  
 KW Signal; Receptor.  
 FT SIGNAL 1  
 SQ SEQUENCE 504 AA; 54567 MW; 16382E57D4276485 CRC64;

## Query Match

Best Local Similarity 81.4%; Score 1448; DB 4; Length 504;  
 Matches 272; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 50 PVEGDPPPLTMTKDGRTIHSGMSRFVLPQGLKVKOVEREDAGVYCKATNGFGLSVN 109  
 |||||||  
 DB 52 PVEGDPPPLTMTKDGRTIHSGMSRFVLPQGLKVKOVEREDAGVYCKATNGFGLSVN 111  
 |||||||  
 QY 110 YTLVVLDDISPGRKSLGPDSSSGQEDPASQOMARPRFTQPSKMRRVIAAPVGSVRLK 169  
 |||||||  
 DB 112 YTLVVLDDISPGRKSLGPDSSSGQEDPASQOMARPRFTQPSKMRRVIAAPVGSVRLK 171  
 |||||||  
 QY 170 CVASGHRPDIITMMKDDQALTRPEAAEPRKKKWTLSLKNRPEDSGKYTCRVSNRAGAIN 229  
 |||||||  
 DB 172 CVASGHRPDIITMMKDDQALTRPEAAEPRKKKWTLSLKNRPEDSGKYTCRVSNRAGAIN 231  
 |||||||  
 QY 230 ATYKVDVIOIRTSKRPVLTGHPVNTVDFGTTSFQCKVRSVDKPYIOWMLKREYGAEGR 289  
 |||||||  
 DB 232 ATYKVDVIOIRTSKRPVLTGHPVNTVDFGTTSFQCKVRSVDKPYIOWMLKREYGAEGR 291  
 |||||||  
 QY 290 HNSTIDVGOKFYVLPFGDWSRPDGSYLKPL 322  
 |||||||  
 DB 292 HNSTIDVGOKFYVLPFGDWSRPDGSYLKPL 324  
 |||||||

RESULT 3  
 Q91288 PRELIMINARY; PRT; 822 AA.  
 AC Q91288;  
 DT 01-NOV-1996 (Tremblrel. 01, Created)  
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)  
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)  
 DE FIBROBLAST GROWTH FACTOR RECEPTOR.  
 OS Pleurodeles waltlilii (Iberian ribbed newt).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Amphibia; Batrachia; Caudata; Salamandroidae; Salamandridae;  
 OC Pleurodeles.



OX NCBI\_TaxID=8319;  
RP  
RN  
SEQUENCE FROM N.A.  
RA MEDLINE=93130775; PubMed=1483392;  
RX Shi D.L., Feige J.U., Rlou J.F., Desmone D.W., Boucaut J.C.;  
"Differential expression and regulation of two distinct fibroblast  
growth factor receptors during early development of the urodele  
amphibian Pleurodeles waltl.";  
RT Development 116:261-273(1992).  
RL  
CC -I- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX  
DOMAIN.  
CC EMBL: X65059; CAA46192.1; -  
DR HSSP: P06239; 3LCK.  
DR InterPro: IPR000719; Euk\_pkinase.  
DR InterPro: IPR003598; Ig\_c2.  
DR InterPro: IPR003006; Ig\_MHC.  
DR InterPro: IPR01245; Tyr\_kin.  
DR Pfam: PF00047; Ig; 3.  
DR Pfam: PF00069; pkinase; 1.  
DR PRINTS: PR00109; TYRKINASE.  
DR SMART: SM00408; IGC2; 3.  
DR SMART: SM00219; TYKC; 1.  
DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE: PS0011; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE: PS00109; PROTEIN\_KINASE\_TYR; 1.  
KW ATP-binding; Transferase; Tyrosine-protein kinase.  
SQ SEQUENCE 822 AA; 92068 MM; 38C4BA4B8C9AB81A CRC64;

Query Match 22.5%; Score 401; DB 13; Length 822;  
Best Local Similarity 32.8%; Pred. No. 3e-26;  
Matches 90; Conservative 58; Mismatches 106; Indels 20; Gaps 7;

OY 61 WTQDRTSHGMSRRVLPGLAKYQVREDAGYVCATNGFSGLSVNTLVLDISP 120  
DB 80 YTESRLQHG--RIRLDTLELADYVEDSGYLQ--VPGTGILINFTISVSDIAS 136  
OY 121 G---KESLGPSSSG--GOEDPASQOMARPTOPSKRRRIARPVGSSVRLKVASGH 175  
DB 137 GDDDEHGRSDSAGDMKEDPPYSTYRAPFWSQPRDKKILYAPAGNTYKFRCPSSGN 196  
OY 176 PRPDITWKKDDQALT--TRPEAEPRKKKWTLSLKNLPEDSGKYTCVSNRAGAINATY 232  
DB 197 PTPGIRMLKNGREFGEGHRIIGIRLRHQWSLVMESVYPSDRGNVTCLEVKKFGSISY 256  
OY 223 KVDVYQRTKRPVLTGTHPVVTITVDFGTTSFQCKVRSVDKRVYQIMKRV-----YGA 287  
DB 257 LLDVLESPHRRPILOAGLPANTTAMLGSDVOFFCKVYSDAOPHIQMLKHIEVNGSRYPD 316  
OY 288 G---RHNSTIDVGQKRFVLPFGDVMWRPDGSY 317  
DB 317 GVPFVQVLKTADINSSEVLYLHNVSFEDAGEY 350

RESULT 4  
O42127 PRELIMINARY; PRT; 802 AA.  
AC O42127;  
DT 01-JAN-1998 (TREMBLrel. 05, Created)  
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
DE FGF RECEPTOR 3.  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;  
OC Xenopodinae; Xenopus.  
OX NCBI\_TaxID=8355;  
RN  
RP  
SEQUENCE FROM N.A.  
RA Honjo I., Kengaku M., Okamoto H.;  
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.  
CC -I- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX  
DOMAIN.

DR EMBL: AB007035; BAA22281.1; -  
DR HSSP: P08631; IAD5.  
DR InterPro: IPR000719; Euk\_pkinase.  
DR InterPro: IPR003598; Ig\_c2.  
DR InterPro: IPR003600; Ig\_like.  
DR InterPro: IPR003006; Ig\_MHC.  
DR InterPro: IPR01245; Tyr\_kin.  
DR Pfam: PF00047; Ig; 3.  
DR Pfam: PF00069; pkinase; 1.  
DR PRINTS: PR00109; TYRKINASE.  
DR SMART: SM00408; IGC2; 2.  
DR SMART: SM00410; IG\_like; 1.  
DR SMART: SM00219; TYKC; 1.  
DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE: PS0011; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE: PS00109; PROTEIN\_KINASE\_TYR; 1.  
KW ATP-binding; Transferase; Tyrosine-protein kinase.  
SQ SEQUENCE 802 AA; 89515 MM; CC5E5DDE3BD25BD3 CRC64;

Query Match 22.3%; Score 396.5; DB 13; Length 802;  
Best Local Similarity 32.9%; Pred. No. 7.1e-26;  
Matches 94; Conservative 49; Mismatches 98; Indels 45; Gaps 9;

OY 45 CAAAPVVEGDDPPPLMTMTKDGRTSHGMSRRVLP-----OG-LKYQVREDAGYV 96  
DB 52 CAAE-----DASTTTKMKDKG-----IGIYNNRTSTROGLIKTIINSSDSDGITS 97  
OY 97 CKATNGFSGLSVNTLVLDISPKESLGPDSSSGQEDPASQOMARPTOPSKMRR 156  
DB 98 CLRMSTELRLNFTIRVTD-----LPSSGDEDDDDDDDETFEDREPRMTQPERMEKK 151  
OY 157 VIARPVGSSVRLKVASGHPDPITWKKDDQALT--RPEAEPRKKKWTLSLKNLPED 213  
DB 152 LIAPAAANTIRRCPAAPNPPTIIMLNKNGREFGEGHRIIGIKLRHQWSLVMESVPSD 211  
OY 214 SGKTCVRSNRAGAINATYKVDVIORTKSKPVLTGTHPVNTVDFGTTSFQCKVRSV 273  
DB 212 KGNITCVYENKYSIRQYQDLVLESSHRLQAGLGNQTVVLGSDVEFFCKYSDAQ 271  
OY 274 PVIQMLKREYGAEGRHNSITDVGQKRFVLPFGDVMWRPDGSYIN 319  
DB 272 PHIQMLKRV-----VNGSKYG--PDGPPYVSVLQSFN 303

RESULT 5  
O918X3 PRELIMINARY; PRT; 800 AA.  
AC O918X3;  
DT 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
DE FIBROBLAST GROWTH FACTOR RECEPTOR 3.  
GN FGFR3.  
OS Brachydanio rerio (Zebrafish) (Zebra danio).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;  
OC Cypriniformes; Cyprinidae; Rasbora; Danio.  
OX NCBI\_TaxID=7955;  
RN  
RP  
SEQUENCE FROM N.A.  
RA Sleptsova-Friedrich I., Li Y., Korzh V., Ge R.;  
RT "The zebrafish fibroblast growth factor receptor 3 (Z-FGFR3) in early  
zebrafish development.";  
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
CC -I- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX  
DOMAIN.  
CC EMBL: AF157560; AAP80344.1; -  
DR InterPro: IPR000719; Euk\_pkinase.  
DR InterPro: IPR003598; Ig\_c2.  
DR InterPro: IPR003006; Ig\_MHC.  
DR InterPro: IPR001245; Tyr\_kin.  
DR Pfam: PF00047; Ig; 3.

DR Pfam: PF00069; pkinase.1  
DR PRINTS: PR00109; TYRKINASE.  
DR SMART: SM00408; IGC2; 3.  
DR SMART: SM00219; TYRC; 1.  
DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
KM ATP-binding: Receptor; Transferase; Tyrosine-protein kinase  
SO SEQUENCE 800 AA; 89716 MW; 8092DC0272A5BAD1 CRC64;

Query Match	22.1%	Score 393;	DB 13;	Length 800;
Best Local Similarity	35.3%	Pred. No. 1.4e-25;		
Matches 84;	Conservative 47;	Mismatches 91;	Indels 16;	Gaps 6

[illegible]

RESULT	6			
099052				
ID	Q99052	PRELIMINARY;	PRT;	800 AA.
AC	Q99052;			
DT	01-JUN-1998 (TrEMBLrel. 06, Created)			
DT	01-JUN-1998 (TrEMBLrel. 06, Last sequence update)			
DT	01-JUN-2001 (TrEMBLrel. 17, Last annotation update)			
DE	FIBROBLAST GROWTH FACTOR RECEPTOR 2 PRECURSOR (Flg-2) (EC 2.7.1.112).			
GN	Flg-2.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=KERATINOCYTES;			
RC	MEDLINE=91296390; PubMed=1648703;			
RA	Atiyl A., Zimmer Y., Yaron A., Yarden Y., Givol D.;			
RT	"Flg-2, a new member of the family of fibroblast growth factor			
RT	receptors.";			
RL	Oncogene 6:1089-1092(1991).			
RN	[2]			
RP	ERRATUM.			
RC	TISSUE=SKIN;			
RA	Atiyl A., Zimmer Y., Yaron A., Yarden Y., Givol D.;			
CC	Oncogene 7:823-823(1992).			
CC	-1- SIMILARITY: BELONGS TO THE FIBROBLAST GROWTH FACTOR RECEPTOR FAMILY.			
CC	-1- SIMILARITY: BELONGS TO THE IMMUGLOBULIN SUPERFAMILY. THE			
CC	EXTRACELLULAR DOMAINS CONTAINS 3 IG-LIKE DOMAINS.			
DR	EMBL: X58255; CAA41209.1; -			
DR	PIR: A60350; A60350.			
DR	HSSP: P12931; 1PMK.			
DR	InterPro: IPR000719; Euk_pkinase.			
DR	InterPro: IPR003598; Ig_c2.			
DR	InterPro: IPR003006; Ig_MHC.			
DR	InterPro: IPR001245; Tyr_kin.			
DR	Pfam: PF00047; Ig_3.			
DR	Pfam: PF00069; pkinase_1.			
DR	PRINTS: PRO0109; TYRKINASE.			
DR	SMART: SM00408; Igc2; 3.			
DR	SMART: SM00219; TYRKC; 1.			

DR		P	PROSITE; PS00107; PROTEIN_KINASE_ATP_1.
DR		P	PROSITE; P850011; PROTEIN_KINSE_DOM_1.
DR		P	PROSITE; PS00109; PROTEIN_KINSE_TYR_1.
KW	Receptor;	G	Glycoprotein; Tyrosine-protein kinase; ATP-binding;
KW	Transferase;	P	Phosphorylation; Transmembrane; Immunoglobulin domain;
KW	Signal.	S	Signal.
FT	SIGNAL.	F	1 20 POTENTIAL.
FT	CHAIN	C	21 800 FIBROBLAST GROWTH FACTOR RECEPTOR 2.
FT	DOMAIN	E	23 369 EXTRACELLULAR.
FT	DOMAIN	I	52 114 IG-LIKE DOMAIN.
FT	DOMAIN	I	163 229 IG-LIKE DOMAIN.
FT	DOMAIN	I	262 340 IG-LIKE DOMAIN.
FT	TRANSMEM	T	370 390 POTENTIAL.
FT	DOMAIN	I	391 800 INTRACELLULAR (CATALYTIC).
FT	NP_BIND	B	468 480 ATP (BY SIMILARITY).
FT	ACT_SITE	A	611 611 ATP (BY SIMILARITY).
FT	BINDING	B	502 502 PHOSPHORYLATION (AUTO-) (BY SIMILARITY)
FT	MOD_RES	M	642 642 N-LINKED (GLCNAG...) (POTENTIAL).
FT	CARBHYD	H	96 96 N-INKED (GLCNAG...) (POTENTIAL).
FT	CARBHYD	H	219 219 N-INKED (GLCNAG...) (POTENTIAL).
FT	CARBHYD	H	256 256 N-INKED (GLCNAG...) (POTENTIAL).
FT	CARBHYD	H	288 288 N-INKED (GLCNAG...) (POTENTIAL).
FT	CARBHYD	H	309 309 N-INKED (GLCNAG...) (POTENTIAL).
FT	CARBHYD	H	322 322 N-INKED (GLCNAG...) (POTENTIAL).
FT	CARBHYD	H	422 422 N-INKED (GLCNAG...) (POTENTIAL).
FT	CARBHYD	H	447 447 N-INKED (GLCNAG...) (POTENTIAL).
EQ	SEQUENCE	S	800 AA; 87691 MW; B37604/TDBEBB312 CRC64;

Query Match	22.0%;	Score 391.5;	DB 4;	Length 800;
Best Local Similarity	31.9%;	Pred. No. 1.9e-25;		
Matches 99;	Conservative 49;	Mismatches 129;	Indels 33;	Gaps 8

QY	5	CCCGCCRRCCGCGP	SHRRPPRRPAPQRMKTRMSHGKWPAGPHCAA-----AVPEGD	54
Db	6	CVLVCAVAVAGAA	SEPPGPAPQVRRRAAEVGPGEPSQEQVAFSGSDTVELSCHPGGA	65
QY	55	PPPLTMTWKDGR	TRHSGMSRRVPLQGLAKVQVREDAQVYVC--KATNGFGLSVYTL	112
Db	66	PLGTVAKKDSTGLVAS--HRLIVBPQRLQVLNASHEDAGVYSCOHRLTR--RYLCHFSV	121	
QY	113	VLDDISPKESLSL	PDSSSGGQEDPASQOARPRFTOPSKMRRVIAIRPVGSSVRLKCA	172
Db	122	RVTDAPESSGDEDE	EDVA---EDTGAPYM-----TRPERMDKKLLAVPAAITYRRFCRA	172
QY	173	SGHRRPITWKKDQAL	T---RPEAAEPKKKKWTLSLKNLPEDSGKYTCRVSNRAGAIN	229
Db	233	QTYVLADVLENSP	HRPILQAGLPANQTAIIISDVEFHCKYVSDAQPHIOMLKHVEVNGSKV	292
QY	285	GAEGRHNSTI	294	
Db	293	CPDCTPYDTV	302	
RESULT	7			
ID	063236	PRELIMINARY;	PRT; 446 AA.	
AC	063236;			
DT	01-NOV-1996 (Tremblrel.	01, Created)		
DT	01-NOV-1996 (Tremblrel.	01, last sequence update)		
DT	01-JUN-2001 (Tremblrel.	17, last annotation update)		
DE	HEPARIN-BINDING FIBROBLAST GROWTH FACTOR RECEPTOR 2 (FRAGMENT).			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OX	NCBI_TaxId=10116;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
SC	TISSUE=PROSTATE;			

RX MEDLINE-93326167; PubMed-8333865;  
 RA Yan G., McBride G., McKeenan W.L.;  
 RT "Exon skipping causes alteration of the COOH-terminus and deletion of  
 RT the phospholipase C gamma 1 interaction site in the FGF receptor 2  
 RT kinase in normal prostate epithelial cells.";  
 RL Biochem. Biophys. Res. Commun. 194:512-518(1993).  
 CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX  
 CC DOMAIN.  
 DR EMBL: L19104; AAA02629.2; -.  
 DR InterPro: IPR003598; Ig\_c2.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR Pfam: PF00047; Ig\_3.  
 DR SMART: SM00408; IGC2; 3.  
 DR Receptor.  
 FT NON\_TER 1 1  
 FT NON\_TER 446 446  
 SQ SEQUENCE 446 AA; 49379 MW; 276DF304DD3080E3 CRC64;  
  
 Query Match 21.8%; Score 387.5; DB 11; Length 446;  
 Best Local Similarity 30.5%; Pred. No. 2.1e-25;  
 Matches 99; Conservative 53; Mismatches 133; Indels 37; Gaps 9;  
  
 QY 23 PPEAPQMRRTMSHGRMPAGPHCAAAVPVSG-----DPEPLTMMTKDGRTHSGMSRF 75  
 Db 62 PEEPTKTYQI-----SQPEACVAVPAGESLELRCKMKDAAVISMTKDG--VHLGPNR 111  
 QY 76 RVL-PQGLKAVQVERDAGVYVCATNGFSGLSVNTLVLDISPGESESGPSSSGGQ 134  
 Db 112 TLVLEIYQIIGANPRPSGLYCAAAARTVSEETLYFMVNVDAISGDEDEDTPSSSEDFV 171  
 QY 135 EDPASQOAWRPFTQPSKMRRTVARIAPGSSVRLKCVASGHPRIDITMMKDDQALT--R 191  
 Db 172 SENSNOBA-PYWNTEKMERLHAVPANVTAKRCRPGGNPTPMRLKNGKEFKOEHR 230  
 QY 192 PEAAPRRKKWTLSLKNLRPESGKYTCRVSNRAGAINATKYVDIORTSKPVLTGTHP 251  
 Db 231 IGRKVRNQHSLMESVPSDKNTYCLVENEGSINHLYHDVESHPRPIQAGLP 290  
 QY 252 VNTTVDEGGTTSPOCKYRSDVKPYIOWLKRYE-----YGAGC-----RHNSTIDVGGQ 299  
 Db 291 ANASTVVGDEYFCKYVSDAQPHIOWIKHEKNGSKYGPDLPLYLKLKHSQ--INSS 347  
 QY 300 KVVLPITGDVMSRPDGSYLK 320  
 Db 348 NAEVLALFNVTEDMAGEYICK 368  
  
 RESULT 8  
 Q9JHX9 PRELIMINARY; PRT: 800 AA.  
 AC Q9JHX9;  
 DT 01-OCT-2000 (Tremblrel. 15, Created)  
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)  
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)  
 DE FIBROBLAST GROWTH FACTOR RECEPTOR 3.  
 GN FGFR3.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OC NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=HANOVER WISTAR;  
 RA Claus P., Grothe C.;  
 RT "Molecular Cloning and Developmental Expression of Rat Fibroblast  
 RT Growth Factor Receptor 3 (FGFR3)."  
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX  
 CC DOMAIN.  
 DR EMBL: AF277717; AAF97795.1; -.  
 DR InterPro: IPR000719; Euk\_pkinase.  
 DR InterPro: IPR003598; Ig\_c2.

DR InterPro: IPR003600; Ig\_1like.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR001245; Tyr\_Kin.  
 DR Pfam: PF00047; Ig\_3.  
 DR Pfam: PF00069; pkinase.1.  
 DR PRINTS: PR00109; TYRKINASE.  
 DR SMART: SM00408; IGC2; 2.  
 DR SMART: SM00410; IG\_Like; 1.  
 DR SMART: SM00219; TYRKc.1.  
 DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP.1.  
 DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM.1.  
 DR PROSITE: PS00109; PROTEIN\_KINASE\_TYR.1.  
 KW ATP-binding; Receptor; Tyrosinase; Tyrosine-protein kinase.  
 SQ SEQUENCE 800 AA; 87674 MW; 128C838A2B990031 CRC64;  
  
 Query Match 21.8%; Score 387; DB 11; Length 800;  
 Best Local Similarity 32.1%; Pred. No. 4.7e-25;  
 Matches 102; Conservative 49; Mismatches 133; Indels 34; Gaps 9;  
  
 QY 5 CCCSCRCRCGSPSHRPPPEAPQMRRTMSHGRMPAGPHCA-----AVPVGD 54  
 Db 6 CVLVCVAVVAGVYSEPPGPOVRGAAEYVGPESQEQVAFSGDPTVELSCHPPGA 65  
 QY 55 PEPITMTTKDGRTHSGMSRFRVL-PQGLKAVQVERDAGVYVC--KATNGFSGLSVNTL 112  
 Db 66 PTGPIPAKKDVGGLVAS-HRLVGPORLOVLNATHEDAGVYSCQORLTR---RVLCHEFSV 121  
 QY 113 VVLDISPGESESGPSSSGGQEDPASQOAWRPFTQPSKMRRTVARIAPGSSVRLKCV 172  
 Db 122 RVTDA PSSGDEDEDGDA-----EDTGAPY-----TRPERMDKLLAVPANTVFERCPA 172  
 QY 173 SGHRPDITMMKDDQALT--RPEAEPKRRKKWTLSLKNLRPESGKYTCRVSNRAGAIN 229  
 Db 173 AGNPPTSIPWLKNGKEFRGHRIGIKLRHOQMSLVMSVPSDGNTCVVENKFGSIR 232  
 QY 230 ATYKVDIORTSKRVLTGTHPVNTTVDEGGTTSPOCKYRSDVKPYIOWLKRYEYAGAGR 289  
 Db 233 QTYTLDVESHPRPIIQAIGLPANQTAVLGSDYFCKYVSDAQPHIOWLKRYEYAGAGR 287  
 QY 290 HNSTIDVGGQREV-VLPT 306  
 Db 288 NGSKVGPDGTPTVTVLKT 305  
  
 RESULT 9  
 Q90749 PRELIMINARY; PRT: 824 AA.  
 AC Q90749;  
 DT 01-NOV-1996 (Tremblrel. 01, Created)  
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)  
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)  
 DE RECEPTOR TYROSINE KINASE.  
 GN BEK.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OC NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-91319411; PubMed-1650446;  
 RA Sato M., Kitazawa T., Iwai T., Seki J., Sakato N., Kato J.Y.,  
 RT Takeya T.;  
 RT "Isolation of chicken-bek and a related gene; identification of  
 RT structural variation in the ligand-binding domains of the FGF-receptor  
 RT family.";  
 RL Oncogene 6:1279-1283(1991).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC Takeya T.;  
 RL Submitted (MAR-1992) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX



CC DOMAIN.  
DR EMBL: X75603: CAA53271.1; -.  
DR HSP, P06239, 3ICK.  
DR InterPro: IPR000719; Euk\_Pkinase.  
DR InterPro: IPR003598; Ig\_C2.  
DR InterPro: IPR003006; Ig\_MHC.  
DR InterPro: IPR001245; Tyr\_Kin.  
DR Pfam: PF00047; Ig\_3.  
DR Pfam: PF00069; Pkinase: 1.  
DR PRINTS: PR00109; TYRKINASE.  
DR SMART: SM00408; IGC2: 3.  
DR SMART: SM00219; TYKIC: 1.  
DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP: 1.  
DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM: 1.  
DR PROSITE: PS00109; PROTEIN\_KINASE\_TYR: 1.  
DR ATP-binding, Transferase, Tyrosine-protein kinase.  
SQ SEQUENCE 796 AA; 88288 MW; 226D99A0B6DD1D92D CRC64;

[illegible]

Qy	174	GHPEDDTMMKDDAL---	RPAAERPRKKWTLSLKLNRBDSGKTCRPSNAGINA	230
		:	:	
	169	GKPPSTWLKNGEPEFGHGLGCIKLRHQMSLMEVSPDNGNTCVVANKYGTIRE	222	
Db				
Qy	231	TYKVDYIQRFSKRVYLGTHTVNTVDPGCTTSQCKRVSDYKVIOMLRKVEYGAAGRH	290	
		:	:	
	229	TYLIDVIERPHRIILDAGFRSNTTVAGSDVEECHKYSDAQHIDIMWLKVE----	281	
Db				

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QY      291 NSTIDVCGQKFEVLLPTGVDVMSRPDGS 316
          | | | |
Db      282 -----VNGSKF-----GPDGN 292

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RESULT	12		
063237			
ID	063237	PRELIMINARY;	PRT; 446 AA.
AC	063237;		
DT	01-NOV-1996 (TREMBLrel. 01, Created)		
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)		
DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)		
DE	HEPARIN-BINDING FIBROBLAST GROWTH FACTOR RECEPTOR 2 (FRAGMENT).		
OS	Rattus norvegicus (Rat).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus		
NCBI	Taxid=10116;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=PROSTATE;		
RX	MEDLINE=93326167; PubMed=8333865;		
RA	Yan G., McBride G., McKeenan W.L.;		
RT	"Exon skipping causes alteration of the COOH-terminus and deletion of		
RT	the phospholipase C gamma 1 interaction site in the FGF receptor 2		
RT	kinase in normal prostate epithelial cells".		
RL	Biochem. Biophys. Res. Commun. 194:512-518(1993).		
CC	-1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLE		
CC	DOMAIN.		
DR	EMBL: L19105; AAA02628.2; .		
DR	InterPro: IPR003598; Ig_c2.		
DR	InterPro: IPR003006; Ig_MHC.		
DR	Pfam: PF00047; 1g; 3.		
DR	SMART: SM00408; 1gc2; 3.		
DR	Receptor.		
DR	1M		

FT	NON_TER	446	446	
SO	SEQUENCE	446 AA;	49249 MW;	A8C3BFD1D7DBB123 CRC64

Query Match	21.6%	Score 383.5	DB 11	Length 446
Best Local Similarity	32.3%	Pred. No. 4	6e-25	
Matches 91	Conservative 48	Mismatches 116	Indels 27	Gaps 7

QY	23	PPKAPQSMRTKMSHGMPACPHCAAAVPVVG-----DPEPLTMTKGGRTIHSQMSRF	75
Db	63	PEEPPTKQI-----SQPEACVYAFGSSLEKMLKDAIVISTKCG--VHLGPNKR	112
QY	76	RVL-PQGLKAYQVERDAGVYVCATNGFGSLSVNTLVLLDDISPKESLAPDSSSGQ	134
Db	113	TVLGEYLIQIKATPRSGISYACAAATVDSFLIYFMVNTDAISGDEDEDDTSSEDFV	172
QY	135	EDPASQOAMRPFRTPQSKMRBYIARVYGSVFLKCVASGHPDQITLWKKDOALL--R	191
Db	173	SEANSNORA-PYMTNTEKMKKRLHANPAAVTYFCRCPAGSNLPPIYKMLKNGKEFQENR	231
QY	192	PEAAEPRKKWTLISLKNLREDSGKYTCRVSNBAGINATYKVDVIQTRTSKRVLTGTHP	251
Db	232	IGGYKVNQHMWSLIMESVNSDGKNTCLVENEYGSINHTYHLDVYERSPHRPIIQAGLP	291
QY	252	VNTITVDEGGTTSPOCKRYSDVKPYIQLKRYE-----YAEAG	288
Db	292	ANASTVVGDDVEFYCKVYSDAQPIQIWKIKHEVNGSKSGPDG	333

RESULT 13	
Q14718	
ID Q14718	PRELIMINARY;
	PRT; 705 AA

DT 01-NOV-1996 (TEMBREl. 01, Created)  
 DT 01-NOV-1996 (TEMBREl. 01, last sequence update)  
 DT 01-JUN-2001 (TEMBREl. 17, last annotation update)  
 DE FIBROBLAST GROWTH FACTOR RECEPTOR (FGFR-2) (EC 2.7.1.112)  
 GN K-SAM-III.  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 NCBI\_TaxID:9606;  
 NX

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RX SEQUENCE FROM N.A.
RA MEDLINE=92212948; PubMed=1313574;
RA Katoch M., Hattori Y., Sasaki H., Tanaka M., Sugano K., Yazaki Y.,
RA Sugimura T., Terada M.;
RT "K-sam gene encodes secreted as well as transmembrane receptor
RT tyrosine kinase.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2960-2964(1992).
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
CC EMBL: M87771; AAA59471.1; -.
DR HSSP: P06239; 3ICR.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR003598; Ig_C2.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR001245; Tyr_kin.
DR Pfam: PF00047; Ig_3.
DR Pfam: PF00069; pkinase_1.
DR PRINTS: PR00109; TRYKINASE.
DR SMART: SM00408; IGC2_2.
DR SMART: SM00219; TYRKC; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PSS0011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
KW ATP-binding; Glycoprotein; Immunoglobulin domain; Phosphorylation;
KW Receptor; Signal; Transferrin; Transmembrane; Tyrosine-protein kinase
FT CHAIN 1 21
FT SIGNAL 1 21 POTENTIAL.
FT CDS 22 705 FIBROBLAST GROWTH FACTOR RECEPTOR 2.
SQ SEQUENCE 705 AA; 79211 MW; 590967DCBF5DA25D CRC64;
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Query Match          21.5%: Score 382.5; DB 4; Length 705;
Best Local Similarity 29.6%: Pred.No.9,8e-25;
Matches 104; Conservative 52; Mismatches 130; Indels 65; Gaps 11.

QY 23 PPEADQRMWTRMSHGMRPAGPHCAAAVPEG-----DPEPLTWTKDGRTIHSGWSRF 75
   | :|:::| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 35 PEPPPTKTYI-----SQPEVYAAPGESLEVRCLKDAAVISWTNG--VHLGPNNR 84
   ||:::| | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 76 RVL-FQGKVKOVEREDAGVYCKATNGSGLSVNTLVLLVDISPGEKSIGPDSSSGGQ 134
   ||:::| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 85 TVLIEGYEQIKATPPDSGLACTASRYTDSFTWFVMNVTVDAISSGD----EDDTDGA 140
   ||:::| | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 135 EDPASO---QMARPRPTQSKMRRRRIARPVASSVRLKVASHGRPRDITNMKKDOALT- 190
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 141 EDFVSSENSNKRKAAPTWTNTERKEKRIHAHPAANYAKFCRPAAGNPPTIRWLKNGEERFQ 200
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 191 --RPEAAPERRKKRWTLSLKNLRPEDSGKYTCVNSNAGAINTYKYVDVIQTFRSPVLTG 248
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 201 EHRRIGCYKVRNQHWSLIMSVPSPDKGNVTCEVENEGSINTHLDVERSRPHRPILQA 260
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 249 TRPVMTYDFGGTTSFQCKVRSADVAPYLQMKRV-----YAEG----- 288
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 261 GLPANASTVVGDDVEFYCVKSYSDAAPHIQIMIKHEKNSGSKYPDGIPLYLKLVSAESS 320
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 289 -----RHNSTID---VGGQKRVVLPDQWSNR-DGSYLNKRL 322
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 321 SNMSTPLVRIITTRLSTADTPMLAGVSEYELEDPEPKWEFPDRKLTLGKPL 371
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 14
OPSV9 PRELIMINARY; PRF; 818 AA.
AC OPSV9.
Dt 01-MAY-2000 (TREMBLrel. 13, Created)
Dt 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
Dr 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE FGF RECEPTOR 4A.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OX NCB1_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Hongo I., Kengaku M., Okamoto H.;
RT "Differential employment of Fgf signaling system for the embryonic
RT induction.";
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
CC -1 SIMILARITY: TO IMMNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN
Cc EMBL; AB007036; BAA22849.1; -.
Dr HSSP; P06239; 3LCK.
Dr InterPro: IPR000719; Euk_pkinase.
Dr InterPro: IPR003598; Ig_c2.
Dr InterPro: IPR003006; Ig_MHC.
Dr InterPro: IPR001245; Tyr_kin.
Dr Pfam; PF00047; Ig_3.
Dr Pfam; PF00069; pkinase; 1.
Dr PRINTS; PRO0109; TYRKINASE.
Dr SMART; SMO0408; IGC2; 3.
Dr SMART; SMO0219; TyrcKc; 1.
Dr PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
Dr PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
Dr PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
KW ATP-binding; Receptor; Transferase; Tyrosine-protein kinase.
SEQUENCE 818 AA; 92067 MW; A8CBA341C9230C1 CRC64;
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[illegible]

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Db 180 PTLPLRMKNGRAFQOQDRIGYKRVSTWLSLINDSVPSDKNGTTCVENEKKAINTTY 239
Oy 233 KVDVIORTSKRPVLTGHPVNTVDGTTSPQCKVRSVDKPVYIOMLKREYGAERHNS 292
Db 240 QLDVVERSPHPILOAGLPANTSVGTAEFSCKVYSDPQPHIOMLKRIE-----NGS 294
Oy 293 TIDVGOKFV-VLPTGDV 309
Db 295 RVASDGFPEYELKTAGV 312

RESULT 16
09DCK3 PRELIMINARY; PRT: 828 AA.
AC 09DCK3;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE FIBROBLAST GROWTH FACTOR RECEPTOR 4C.
GN FGFR-4C.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=11180841;
RA Golub R., Adelman Z., Clement J., Weiss R., Bonasera J.,
RA Servetnick M.;
RT "Evolutionarily conserved and divergent expression of members of the
RT FGF receptor family among vertebrate embryos, as revealed by FGFR
RT expression patterns in Xenopus.";
RL Dev. Genes Evol. 210:345-357(2000).
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL: AF288453; AAG01013.1; -.
DR InterPro: IPR000719; Euk_Pkinase.
DR InterPro: IPR003598; Ig_Pkinase.
DR InterPro: IPR003598; Ig_c2.
DR InterPro: IPR003600; Ig_Like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR002290; Ser Thr_kin_actsite.
DR InterPro: IPR001245; Tyr_kin.
DR Pfam: PF00047; Ig; 3.
DR Pfam: PF00069; Pkinase; 1.
DR PRINTS: PR00109; TYRKINASE.
DR SMART: SM00408; IGC2; 3.
DR SMART: SM00410; IGC2; 3.
DR SMART: SM00410; IG_Like; 2.
DR SMART: SM00220; S_TKc; 1.
DR SMART: SM00219; TYRKc; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR ATP-binding: Receptor: Transferrase
KW SEQUENCE 828 AA; 93211 MW; 72E205263505E323 CRC64;

Query Match 21.3%; Score 378.5; DB 13; Length 828;
Best Local Similarity 32.5%; Pred. No. 2,7e-24;
Matches 86; Conservative 51; Mismatches 103; Indels 25; Gaps 8;
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```
Db 195 PAGSPPLTIMKNGRFRGHRIGIQRHQHSLMESVPSDRGNTCVENRYGS 254
Oy 228 INATYKVDVIORTSKRPVLTGHPVNTVDGTTSPQCKVRSVDKPVYIOMLKREYGAER 287
Db 225 LTYTFELDLVERSSHRPILQAGLPANTARVGSDFEYCKVYSDAPQPHIOMLKRIE--VN 312
Oy 288 GRHNSTIDVGOKF--VLPTGDV 309
Db 313 GSH-----FGPDPEFYVYLKTADI 332

RESULT 17
091742 PRELIMINARY; PRT: 818 AA.
AC 091742;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE FIBROBLAST GROWTH FACTOR RECEPTOR 4 PRECURSOR (FGFR-4) (EC 2.7.1.112).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95137391; PubMed=7835703;
RA Shiozaki C., Tashiro K., Asano-Miyoshi M., Saijo K., Emori Y.,
RA Shiozaki K.;
RT "Cloning of cDNA and genomic DNA encoding fibroblast growth factor
RT receptor-4 of Xenopus laevis.";
RL Gene 152:215-219(1995).
CC -1- FUNCTION: RECEPTOR FOR ACIDIC FIBROBLAST GROWTH FACTOR. DOES NOT
CC BIND TO BASIC FIBROBLAST GROWTH FACTOR.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- DEVELOPMENTAL STAGE: IT IS A MATERNAL PROTEIN WHICH DECREASES
CC GRADUALLY TO THE LATE BLASTULA STAGE AND THEN INCREASES BY ZYGOTIC
CC EXPRESSION REACHING A MAXIMUM AT THE BLASTULA AND THE LATE
CC GASTRULA STAGES.
CC -1- SIMILARITY: BELONGS TO THE FIBROBLAST GROWTH FACTOR RECEPTOR
CC FAMILY.
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. THE
CC EXTRACELLULAR DOMAINS CONTAINS 3 IG-LIKE DOMAINS.
DR EMBL: D31761; BAA06539.1; -.
DR HSP; P06239; 3ICK.
DR InterPro: IPR000719; Euk_Pkinase.
DR InterPro: IPR003598; Ig_c2.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR001245; Tyr_kin.
DR Pfam: PF00047; Ig; 3.
DR Pfam: PF00069; Pkinase; 1.
DR PRINTS: PR00109; TYRKINASE.
DR SMART: SM00408; IGC2; 3.
DR SMART: SM00219; TYRKc; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_TYR; 1.
DR Receptor: Glycoprotein; Tyrosine-protein kinase; ATP-binding;
KW Receptor; Glycoprotein; Tyrosine-protein kinase; Immunoglobulin domain;
KW Transferrase; Phosphorylation; Transmembrane; Immunoglobulin domain;
KW Signal.
FT CHAIN 1 26 POTENTIAL.
FT 27 818 FGF RECEPTOR 4. (POTENTIAL).
FT TRANSSEM 27 381 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 382 402 POTENTIAL.
FT DOMAIN 403 818 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 56 115 IG-LIKE DOMAIN.
FT DOMAIN 177 243 IG-LIKE DOMAIN.
FT DOMAIN 276 352 IG-LIKE DOMAIN.
FT DOMAIN 479 767 PROTEIN KINASE.
FT NP_BIND 485 493 ATP (BY SIMILARITY).
FT BINDING 515 515 ATP (BY SIMILARITY).
FT AC_SITE 624 624 BY SIMILARITY.
FT MOD_RES 655 655 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
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Db 201 EHRIGGYVRNQHWSLIMESVPSDKNGYTCVENDYGINHTYHLDVRSRPHRLQA 260  
QY 249 THPVNTVDFGCTTSFOCKVRSDVKPVIOMLKRE-----YGAEG-----RHNSTIDV 296  
Db 261 GLPNASTYVGGDVEFCVKYSDAOPHIOMIKHEKNGSKYGPDLPLYLKLKHS---I 317  
QY 297 GGQKFEVLPFGDWSRPGSYLNK 320  
Db 318 NSSNAEVLALFNVTADAGEYICK 341  
RESULT 20  
012922  
ID 012922; PRELIMINARY; PRT; 366 AA.  
AC 012922;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
DE SOLUBLE KERATINOCYTE GROWTH FACTOR RECEPTOR PRECURSOR (BC 2.7.1.112).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE-BREAST, AND CORNEA.  
RX MEDLINE=95170769; Pubmed=7866434;  
RA Wilson S.E., Weng J., Chwang E.L., Gollahon L., Leitch A.M.,  
RA Shay J.W.;  
RT "hepatocyte growth factor (HGF), keratinocyte growth factor (KGF), and  
RT their receptors in human breast cells and tissues: alternative  
RT receptors";  
RL Cell. Mol. Biol. Res. 40:337-350(1994).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE-BREAST, AND CORNEA.  
RX MEDLINE=92108030; Pubmed=1309608;  
RA Miki T., Bottaro D.P., Fleming T.P., Smith C.L., Burgess W.H.,  
RA Chan A.M., Aaronson S.A.;  
RT "Determination of ligand-binding specificity by alternative splicing:  
RT two distinct growth factor receptors encoded by a single gene";  
RL Proc. Natl. Acad. Sci. U.S.A. 89:246-250(1992).  
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX  
DOMAIN.  
DR EMBL: U11814; AAA68514.1; -  
DR InterPro: IPR003598; Ig\_c2.  
DR InterPro: IPR003598; Ig\_c2.  
DR Pfam: PF00047; Ig; 3.  
DR SMART: SM00408; IGC2; 3.  
KW Receptor; Glycoprotein; Immunoglobulin domain; Signal; Keratin.  
FT SIGNAL 1 21  
FT CHAIN 22 366  
FT DOMAIN 55 114  
FT DOMAIN 172 238  
FT DOMAIN 271 349  
FT DISULFID 62 107  
FT DISULFID 179 231  
FT DISULFID 278 340  
FT CARBOHYD 83 123  
FT CARBOHYD 123 123  
FT CARBOHYD 228 228  
FT CARBOHYD 241 241  
FT CARBOHYD 265 265  
FT CARBOHYD 297 297  
FT CARBOHYD 318 318  
FT CARBOHYD 331 331  
SQ SEQUENCE 366 AA; 40614 MW; C02708836203465F CRC64;

QY 23 PPEAQRRTNRSHGRMPAGPCHCAAVPEG-----DPEPLTMTKDGRTIHSGMSRF 75  
Db 35 PEEPTKTOI-----SQPEVYVAAPGESLEVRCLLKDAAVISMTKG--VHLGPNNR 84  
QY 76 RVL-FOGLKVRKOVEREDAGVYCKATNGFSLSVNTVLVLDLDSPEKESLGPDSGSGQ 134  
Db 85 TVLIGIEYLQIKGATPRDSGLVACTASRTYVDSFTWTFMNVTDALISSGD---EDDTGA 140  
QY 135 EDPASQ---QMARPRETOPSKMRRIYARPGSSVRLCVASGAPRPDITMKDQALTL- 190  
Db 141 EDFVSESNENNRKAPYWTETKEKERRLHVAANVTAKVFCRCPAGCNPMPTMRMLKNGKEFKO 200  
QY 191 --RPAARPRKKKWTLSLKNLRPDSCKYTCVSRACAINTYKVDYQRTSRPVLTG 248  
Db 201 EHRIGGYVRNQHWSLIMESVPSDKNGYTCVENDYGINHTYHLDVRSRPHRLQA 260  
QY 249 THPVNTVDFGCTTSFOCKVRSDVKPVIOMLKRE-----YGAEG-----RHNSTIDV 296  
Db 261 GLPNASTYVGGDVEFCVKYSDAOPHIOMIKHEKNGSKYGPDLPLYLKLKHS---I 317  
QY 297 GGQKFEVLPFGDWSRPGSYLNK 320  
Db 318 NSSNAEVLALFNVTADAGEYICK 341  
RESULT 21  
090IH3  
ID 090IH3; PRELIMINARY; PRT; 768 AA.  
AC 090IH3;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
DE K-SAM-1103.  
DE K-SAM.  
GN K-SAM.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Ueda T., Sasaki H., Kuwahara Y., Nezu M., Shibuya T., Sakamoto H.,  
RA Ishii H., Yanagihara K., Mafune K., Makuchi M., Terada M.;  
RT "Deletion of the carboxyl-terminal exons of k-sam/FGFR2 by short  
RT homology-mediated recombination, generating preferential expression of  
RT specific mRNAs";  
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.  
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX  
DOMAIN.  
DR EMBL: AB030078; BAA89301.1; -  
DR HSSP: P12931; IEWK.  
DR InterPro: IPR000719; Euk\_pkinase.  
DR InterPro: IPR003598; Ig\_c2.  
DR InterPro: IPR003598; Ig\_c2.  
DR InterPro: IPR001245; Tyr\_kin.  
DR Pfam: PF00047; Ig; 3.  
DR Pfam: PF00069; pkinase; 1.  
DR PRINTS: PR00109; TYRKINASE.  
DR SMART: SM00219; TYRK; 1.  
DR SMART: SM00408; IGC2; 3.  
DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE: PS00109; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE: PS00109; PROTEIN\_KINASE\_TYR; 1.  
KW ATP-binding; Transferase; Tyrosine-protein kinase.  
SQ SEQUENCE 768 AA; 86208 MW; A6F1A35DD69FAAAA CRC64;

Query Match 21.1%; Score 375.5; DB 4; Length 768;  
Best Local Similarity 29.9%; Pred. No. 4.4e-24;  
Matches 97; Conservative 55; Mismatches 129; Indels 43; Gaps 10;

QY 23 PPEAQRRTNRSHGRMPAGPCHCAAVPEG-----DPEPLTMTKDGRTIHSGMSRF 75  
Matches 97; Conservative 55; Mismatches 129; Indels 43; Gaps 10;

Db 35 PEEPTKYOI-----SOPEVYVAAPGESLEVERCLLKDAVAISWTKDG--VHLGPNR 84  
QY 76 RVL-POGLKVKOVEREDAGVYVCKATNGFSLSNVTLVLDISPCKESIGPSSSGGQ 134  
Db 85 TVLIGETLQIKGATPRDSGLACTASRTVDSWTYFMVNTDAISSGD---EDDTDGA 140  
QY 135 EDPASQ---OWARPRFTOPSMMRRRVIAIPVSSSVRLKCVASGHPRPDITWKKDQALT- 190  
Db 141 EDFESENSNNKRAPYWNTEKMERKRLHAPAAVNTVRCRCAGGPNMTMRLKNGKFERQ 200  
QY 191 --REAAEPKKKWTLSLKNLRPEDSGKYTCRVSNRAGAINATYKVDVIOFTNSKPYLTG 248  
Db 201 EHRIGYKVRNQHMSLIMESVSPDKNGYTCVENEYGSINHYYHLIDVERSHPRILOA 260  
QY 249 THPNTVTVDGCGTSPFCCKVRSVDKPYIOMLKRYE-----YGAGS-----RHNSITDV 296  
Db 261 GLPNASTVVGDDVEFCCKYSDAOPHIOMIKHVEKNGSKYGPDLPLYLKXHSG---I 317  
QY 297 GGGKFEVVLPTGDVWSRPDGSYLK 320  
Db 318 NSSNAEVLALFNVTADAGEYICK 341

RESULT 22  
Q90TH5 PRELIMINARY; PRT; 771 AA.  
AC Q9U1H5; 01-MAY-2000 (TReMBLrel. 13, Created)  
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
DE 01-JUN-2001 (TReMBLrel. 17, Last annotation update)  
GN K-SAM-1101.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Ueda T., Sasaki H., Kuwahara Y., Nezu M., Shibuya T., Sakamoto H.,  
RA Ishii H., Yanagihara K., Matune K., Makuchi M., Terada M.;  
RT "Deletion of the carboxyl-terminal exons of K-sam/GGFR2 by short  
RT homology-mediated recombination, generating preferential expression of  
RT specific mRNAs.";  
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.  
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX  
CC DOMAIN.  
DR EMBL; AB030076; BAA89299.1; -.  
DR HSSP; P12931; IFMK.  
DR InterPro; IPR000719; Euk\_pkinase.  
DR InterPro; IPR003598; Ig\_C2.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR001245; Tyr\_kin.  
DR Pfam; PF00047; Ig\_3.  
DR Pfam; PF00069; pkinase.1.  
DR PRINTS; PR00109; TYRKINASE.  
DR SMART; SM00408; Igc2; 3.  
DR SMART; SM00219; Tyrc; 1.  
DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE; PS00111; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.  
KW ATP-binding; Transferase; Tyrosine-protein kinase.  
SQ SEQUENCE 771 AA; 86505 MW; BFC73746F1A35DD6 CRC64;

Query Match 21.1%; Score 375.5; DB 4; Length 771;  
Best Local Similarity 29.9%; Pred. No. 4.4e-24;  
Matches 97; Conservative 55; Mismatches 129; Indels 43; Gaps 10;

QY 23 PEPAPQRMTRNSHGKWPAGPHCAAVPEG-----DPPILMTWKDGRTHSGWSRF 75  
Db 35 PEEPTKYOI-----SOPEVYVAAPGESLEVERCLLKDAVAISWTKDG--VHLGPNR 84  
QY 76 RVL-POGLKVKOVEREDAGVYVCKATNGFSLSNVTLVLDISPCKESIGPSSSGGQ 134  
Db 76 RVL-POGLKVKOVEREDAGVYVCKATNGFSLSNVTLVLDISPCKESIGPSSSGGQ 134

Db 85 TVLIGETLQIKGATPRDSGLACTASRTVDSWTYFMVNTDAISSGD---EDDTDGA 140  
QY 135 EDPASQ---OWARPRFTOPSMMRRRVIAIPVSSSVRLKCVASGHPRPDITWKKDQALT- 190  
Db 141 EDFESENSNNKRAPYWNTEKMERKRLHAPAAVNTVRCRCAGGPNMTMRLKNGKFERQ 200  
QY 191 --REAAEPKKKWTLSLKNLRPEDSGKYTCRVSNRAGAINATYKVDVIOFTNSKPYLTG 248  
Db 201 EHRIGYKVRNQHMSLIMESVSPDKNGYTCVENEYGSINHYYHLIDVERSHPRILOA 260  
QY 249 THPNTVTVDGCGTSPFCCKVRSVDKPYIOMLKRYE-----YGAGS-----RHNSITDV 296  
Db 261 GLPNASTVVGDDVEFCCKYSDAOPHIOMIKHVEKNGSKYGPDLPLYLKXHSG---I 317  
QY 297 GGGKFEVVLPTGDVWSRPDGSYLK 320  
Db 318 NSSNAEVLALFNVTADAGEYICK 341

RESULT 23  
Q90TH4 PRELIMINARY; PRT; 817 AA.  
AC Q9U1H4; 01-MAY-2000 (TReMBLrel. 13, Created)  
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
DE 01-JUN-2001 (TReMBLrel. 17, Last annotation update)  
GN K-SAM-1102.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Ueda T., Sasaki H., Kuwahara Y., Nezu M., Shibuya T., Sakamoto H.,  
RA Ishii H., Yanagihara K., Matune K., Makuchi M., Terada M.;  
RT "Deletion of the carboxyl-terminal exons of K-sam/GGFR2 by short  
RT homology-mediated recombination, generating preferential expression of  
RT specific mRNAs.";  
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.  
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX  
CC DOMAIN.  
DR EMBL; AB030077; BAA89300.1; -.  
DR HSSP; P12931; IFMK.  
DR InterPro; IPR000719; Euk\_pkinase.  
DR InterPro; IPR003598; Ig\_C2.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR001245; Tyr\_kin.  
DR Pfam; PF00047; Ig\_3.  
DR Pfam; PF00069; pkinase.1.  
DR PRINTS; PR00109; TYRKINASE.  
DR SMART; SM00408; Igc2; 3.  
DR SMART; SM00219; Tyrc; 1.  
DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE; PS00111; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.  
KW ATP-binding; Transferase; Tyrosine-protein kinase.  
SQ SEQUENCE 817 AA; 91718 MW; A84ED3EFBD0D1B77 CRC64;

Query Match 21.1%; Score 375.5; DB 4; Length 817;  
Best Local Similarity 29.9%; Pred. No. 4.7e-24;  
Matches 97; Conservative 55; Mismatches 129; Indels 43; Gaps 10;

QY 23 PEPAPQRMTRNSHGKWPAGPHCAAVPEG-----DPPILMTWKDGRTHSGWSRF 75  
Db 35 PEEPTKYOI-----SOPEVYVAAPGESLEVERCLLKDAVAISWTKDG--VHLGPNR 84  
QY 76 RVL-POGLKVKOVEREDAGVYVCKATNGFSLSNVTLVLDISPCKESIGPSSSGGQ 134  
Db 85 TVLIGETLQIKGATPRDSGLACTASRTVDSWTYFMVNTDAISSGD---EDDTDGA 140

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OY 135 EDPASQ---QNAARPFPTQPSKRRRVINARPPVSSVRLKCVASGHRPRDITWKKDDQALT- 190
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
Db 141 EDVSENSNNKRAPRPTWTEKMEKRLHVPANPAITVFKRCPAGGNPMPTRMLKNGKEFEKQ 200
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
OY 191 --RPEAAPRRKKWTLSTLKNLPRDESGKYTCVSNRAGAINATVYKVDVIOPTRRSPVLTG 248
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
Db 201 EHRIGCYKVRNQHNSLKLINESVPSKQKNTCVLENYEGSSINTTYILDYERSPHRPIIDA 260
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
OY 249 THPVNTVDFEGTTSFEQGVNSDVKPVITQWLKRYE----YGAEG-----RHNSTIDV 296
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
Db 261 GLPANAATVYGVGDVEFYCVKYSADAPHIQIWKIHKENKSKYGPDLPLFKLVKLKHSQ---I 317
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
OY 297 GQGRFVPLPTGDVWSPRDSYLNK 320
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
Db 318 NSSNAEVLALFNVTEDADAGEYICK 341
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : :

RESULT 24
O9UIH8 PRELIMINARY; PRT; 819 AA.
AC O9UIH8;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE K-SAM-11H1.
GN K-SAM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A.
RP Ueda T., Sasaki H., Kuwahara Y., Nezu M., Shibuya T., Sakamoto H.,
RA Ishii H., Yanagihara K., Mañone K., Makuchi M., Terada M.:
RT "Deletion of the carboxyl-terminal exons of K-sam/EGFR2 by short
RT homology-mediated recombination, generating preferential expression of
RT specific mRNAs."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; AB030073; BAA09296.1; -.
DR HSSP; P12931; IEMK.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR001245; Tyr_kin.
DR Pfam; PF00047; Ig_3.
DR Pfam; PF00069; pkinase.1.
DR PRINTS; PR00109; TYRKINASE.
DR SMART; SM00408; IGC2; 3.
DR SMART; SM00219; TYRC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR ATP-binding; Transferrase; Tyrosine-protein kinase.
KW SEQUENCE 819 AA; 91664 MM; D2A4EB6A6ABA6EE CRC64;

Query Match 21.18; Score 375.5; DB 4; Length 819;
Best Local Similarity 29.98; Pred. No. 4.8e-24;
Matches 97; Conservative 55; Mismatches 129; Indels 43; Gaps 10;

OY 23 PPEAORRRTMSHGRCWPGPHCAAVVEG-----DPPPLVMTWKDGRTHSGWMSRF 75
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
Db 35 PEEPTTKQI-----SPEYVYAAAGESLEVCCLKDAVAIVMTKQG--VHLGPNKR 84
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
OY 76 RVL-PQGLKVRQVEREDAGVYVCAKTNFGSLVSVYTTLVLDIDISPGKESLGPDSSSGQ 134
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
Db 85 TYLLIEGLQIKAGPRDSGLVACTASRTVDSSTVEFVNVVTAISSGD---EDDTQGA 140
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
OY 135 EDPASQ---QNAARPFPTQPSKRRRVINARPPVSSVRLKCVASGHRPRDITWKKDDQALT- 190
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
Db 141 EDVSENSNNKRAPRPTWTEKMEKRLHVPANPAITVFKRCPAGGNPMPTRMLKNGKEFEKQ 200
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : :

```

Oy	191	--RPAABPRKKKMTLSKLNLRPEDSGKYTCVSRNAGAINATYVDVIOFRSRKPVLTG	248
Db	201	EHRIIGCYVRNDQMSLINESVPSDKNGTTCVENETGSIINTYTHLDVSRPHPILOA	260
Oy	249	THPVVTVDFGCTGSFQCKKRSRSDVPVIOWLKRV-----YGAEG-----RHNSTIDV	296
Db	261	GLPAAASVYVGDDVEFCVKYSDAPHLIOWKHVEKNSKSGPDPLLPLKYLKSHG---I	317
Oy	297	GGQKRVVLEPTGDVWSRPDGSYLNK	320
Db	318	NSSNAEVLALFNVTEDADAGEYICK	341
RESULT	25		
Q9UIH7	Q9UIH7	PRELIMINARY; PRT. 819 AA.	
AC	Q9UIH7		
DT	01-MAY-2000 (TREMBLrel. 13, Created)		
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)		
DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)		
DE	K-SAM-11H2 (FRAGMENT).		
GN	K-SAM.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
OX	NCBI_TaxId=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Ueda T., Sasaki H., Kuwahara Y., Nezu M., Shibuya T., Sakamoto H.,		
RA	Ishii H., Yanagihara K., Mafune K., Makuuchi M., Terada M.;		
RT	"Deletion of the carboxyl-terminal exons of K-sam/GFR2 by short		
RT	homology-mediated recombination, generating preferential expression of		
RT	specific mRNAs."		
RL	Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.		
CC	-1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX		
CC	DOMAIN.		
DR	EMBL: AB030074; BAA89297.1; -		
DR	HSSP: P12931; IEMK.		
DR	InterPro: IPR000719; Euk_dkinase.		
DR	InterPro: IPR003598; I9_C2.		
DR	InterPro: IPR003006; I9_MHC.		
DR	InterPro: IPR001245; Tyr_kin.		
DR	Pfam: PF00047; I9; 3.		
DR	Pfam: PF00069; pkinase; 1.		
DR	PRINTS: PR00109; TYRKINASE.		
DR	SMART: SM00408; IGC2; 3.		
DR	SMART: SM00219; TYRC; 1.		
DR	PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.		
DR	PROSITE: PS0011; PROTEIN_KINASE_DOM; 1.		
DR	PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.		
KW	ATP-binding; Transferase; Tyrosine-protein kinase.		
KW	FT		
FT	NON_TER	819	
FT	SEQUENCE	819 AA; 91739 MM; 52D5955E7B76F4D9 CRC64;	
Qy	Query Match	21.1%; Score 375.5; DB 4; Length 819;	
Qy	Best Local Similarity	29.9%; Pred. 4.8e-24;	
Qy	Matches	97; Conservative 55; Mismatches 129; Indels 43; Gaps 10;	
Db	23	PEAPQRMRTSRHSGMPGPHCAAVVEG-----DPEPLTMWTRDGRTHSGMSRF	75
Db	35	PEEPPTKQI-----SQPEVYVAAAGESLEFVCLKDAIVSTWTDG--VHLGPMNR	84
Oy	76	RVL-PQGLKVRQVEREDAGVYVCAKATNGFGLSVNYTLVLVDLSDISPGKESLGPOSSSGGQ	134
Db	85	TVLLIEYLIQIKGATPRDSDGLYACTASRFVDSSTWYFMVNTDAISSGDD---EDDTGA	140
Oy	135	EDPASQ---QMARPEFTQPSKMRRRVITARPVGSSVRLKCVASGHRPRDITWKKDOALT-	190
Db	141	EDPVSNSNNKRAPLWITETKMEKRLHVAIPAANTYKFCPPAGGNMPTMYRLKNGKEKQ	200
Oy	191	--RPAABPRKKKMTLSKLNLRPEDSGKYTCVSRNAGAINATYVDVIOFRSRKPVLTG	248

Db 201 EHRIGGYKVNQHMSLIMESVPSDKNTVCVVENEXGSINHTYHLDVVERSPHPIQA 260  
QY 249 THEVNTTVDGCGTTSFQCKYRSDVKPVICWLRKE-----YGABG-----RHNSTIDY 296  
Db 261 GUPANASTVVGDDVEVCVKYSDAQPHIOWIKHVEKNKSKYPPDGLPYLKLKHSG--I 317  
QY 297 GGOKFVVLPTGDVWSRPDGSYLNK 320  
Db 318 NSSNAEVLALFNVTADAGEYICK 341

Search completed: May 2, 2002, 08:53:26  
Job time: 202 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

## OM protein - protein search, using sw model

Run on: May 2, 2002, 08:48:38 ; Search time 16.07 Seconds

(without alignments)  
1526.335 Million cell updates/sec

Title: US-09-823-038a-33

Sequence: 1 RRAPCCSCRCRCMCPSHR.....VLPTGDVMSRPDGSYLNKPL 322

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

PIR-68:  
1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	401	22.5	822	2	B49151 fibroblast growth
2	395	22.2	822	2	S19947 fibroblast growth
3	391.5	22.0	800	1	TVH02F fibroblast growth
4	391	22.0	801	2	A48991 heparin-binding gr
5	391	22.0	801	2	I55363 fibroblast growth
6	386	21.7	824	2	S24108 protein-tyrosine k
7	384.5	21.6	822	2	B54846 fibroblast growth
8	384	21.6	797	2	S38579 fibroblast growth
9	382	21.5	823	2	B35963 protein-tyrosine k
10	381.5	21.4	812	1	A36477 fibroblast growth
11	378	21.2	806	1	TVH0P3 fibroblast growth
12	377	21.2	818	2	JC4058 fibroblast growth
13	375.5	21.1	769	2	S16236 fibroblast growth
14	375.5	21.1	806	2	A35963 protein-tyrosine k
15	375.5	21.1	822	2	A45081 fibroblast growth
16	375.5	21.1	822	2	JC4583 keratinocyte growt
17	374	21.0	829	2	JC4583 fibroblast growth
18	371.5	20.9	821	1	TVH0P2 fibroblast growth
19	368.5	20.7	814	1	A39752 fibroblast growth
20	368.5	20.7	821	1	TVMSBK fibroblast growth
21	364.5	20.5	822	2	I49289 fibroblast growth
22	363	20.4	480	2	A56182 fibroblast growth
23	362.5	20.4	802	2	TVH0P4 fibroblast growth
24	362.5	20.4	822	2	S29840 fibroblast growth
25	362	20.3	480	2	B56182 fibroblast growth
26	362	20.3	832	2	JH0393 fibroblast growth
27	360.5	20.3	662	2	C40862 heparin-binding gr
28	360.5	20.3	822	1	TVH0P3 fibroblast growth
29	358.5	20.2	799	2	S18209 fibroblast growth

30	358.5	20.2	819	1	TVCHRG fibroblast growth
31	356.5	20.0	361	2	PM0020 fibroblast growth
32	356.5	20.0	824	2	S36439 fibroblast growth
33	355.5	20.0	820	2	S17295 fibroblast growth
34	354	19.9	816	2	A49151 fibroblast growth
35	353.5	19.9	822	1	TVMSFG fibroblast growth
36	334.5	18.8	813	1	A49123 fibroblast growth
37	324	18.2	353	2	S51242 heparin-binding fi
38	318	17.9	682	2	A35969 heparin-binding gr
39	315	17.7	713	2	I50128 fibroblast growth
40	307	17.3	707	2	A54846 fibroblast growth
41	307	17.3	707	2	A38429 keratinocyte growt
42	307	17.3	729	2	A56795 fibroblast growth
43	305	17.1	733	2	I49293 fibroblast growth
44	304	17.1	302	2	C36464 fibroblast growth
45	304	17.1	705	2	S51635 fibroblast growth
46	283.5	15.9	748	2	S41050 fibroblast growth
47	283.5	15.9	750	2	S41051 fibroblast growth
48	282	15.9	650	1	JC1450 fibroblast growth
49	257	14.4	254	1	C42691 fibroblast growth
50	254	14.3	2029	1	TDFFLK protein-tyrosine-p
51	243.5	13.7	790	2	A39627 protein-tyrosine k
52	243.5	13.7	1052	2	B49120 protein-tyrosine k
53	237	13.3	1612	2	T30805 duttl protein - mo
54	234.5	13.2	483	2	T17346 hypothetical prote
55	233	13.1	423	2	T29549 hypothetical prote
56	233	13.1	1273	2	T42405 sax-3 protein - Ca
57	232.5	13.1	5175	2	T20992 hypothetical prote
58	232.5	13.0	5198	2	T43290 hemocentin precurs
59	230.5	12.9	946	1	AA7299 ror-related recept
60	230	12.7	1651	2	T14160 transmembrane rece
61	226.5	12.7	4391	2	A38096 perlecan precursor
62	225	12.6	1239	1	A32579 neuroglian - fruit
63	224	12.6	3707	2	S18252 heparan sulfate pr
64	221.5	12.5	729	2	A49120 fibroblast growth
65	220	12.4	1344	2	T14316 lig-1 protein - mo
66	218.5	12.3	6642	2	T29757 protein UNC-89 - C
67	213.5	12.0	1256	2	T03096 CDO protein - rat
68	210.5	11.8	1091	2	A58332 glial cell membran
69	209.5	11.8	1033	2	S19247 receptor tyrosine
70	208	11.7	1040	2	A57638 hypothetical prote
71	208	11.7	1103	2	T22889 tumor suppressor p
72	207	11.6	1447	2	A54100 projectin - fruit
73	206.5	11.6	6658	2	T13931 protein-tyrosine k
74	206	11.6	871	1	I48696 protein-tyrosine k
75	206	11.6	881	1	I48697 tumor suppressor -
76	205.5	11.6	1427	2	I51669 KIRAO992 protein -
77	205	11.5	772	2	T13078 CDO protein - huma
78	204	11.5	1240	2	T03097 protein-tyrosine-p
79	204	11.5	1501	2	I58148 protein-tyrosine-p
80	204	11.5	1863	2	S46217 protein-tyrosine-p
81	203	11.4	1907	2	S50893 protein-tyrosine-p
82	202.5	11.4	1040	2	A34695 axonal glycoprotei
83	202	11.4	1272	2	S26180 neurofascin - chic
84	202	11.4	1499	2	I50212 protein-tyrosine-p
85	201.5	11.3	1020	2	S05944 neuronal cell surp
86	201.5	11.3	1912	2	A56178 protein-tyrosine-p
87	201.5	11.3	2541	2	T29340 hypothetical prote
88	201.5	11.3	2783	2	T34416 hypothetical prote
89	201	11.3	4162	2	T42633 connectin/titin -
90	200	11.2	1262	1	B48758 protein-tyrosine-p
91	200	11.2	1496	2	A48758 protein-tyrosine-p
92	200	11.2	1896	2	T08851 Down syndrome cell
93	199.5	11.2	853	1	I180NC neural cell adhesi
94	199	11.2	1277	2	T30532 neural cell adhesi
95	199	11.2	1375	2	T13822 frazzled gene prot
96	199	11.2	1526	2	T13823 frazzled gene prot
97	198.5	11.2	1018	2	JC4211 neural adhesion pr
98	198.5	11.2	1894	2	C54689 protein-tyrosine-p
99	197.5	11.1	1018	2	A54744 contactin 1 precur
100	196.5	11.0	1021	2	A57112 contactin precursor





R:Sato, M.; Kitazawa, T.; Iwai, T.; Seki, J.; Sakato, N.; Kato, J.; Takeya, T.

Oncogene 6, 1279-1283, 1991

A:Title: Isolation of chicken-bek and a related gene; identification of structural variants

A:Reference number: S24108; MUID:91319411

A:Accession: S24108

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-824 <SAT>

C:Cross-references: EMBL:X61992; NID:963085; PIDN:CA03965.1; PID:963086

C:Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; protein kinase

C:Keywords: ATP; growth factor receptor; phosphotransferase; tyrosine-specific protein kinase

F:174-235/Domain: immunoglobulin homology <IMM>

F:482-767/Domain: protein kinase homology <KIN>

F:490-498/Region: protein kinase ATP-binding motif

Query Match 21.7%; Score 386; DB 2; Length 824;

Best Local Similarity 29.3%; Pred. No. 6.9e-20;

Matches 97; Conservative 59; Mismatches 117; Indels 58; Gaps 11;

23 PPEAPORWRTWMSHGRWPCPHCAAVVEGDPPL-----TWTKDG-----R 66

38 PPEPPTKYQI-----SQPDVHSALP--GEPELKCQLKDAVMISWTKDGVPLGPDNR 87

67 THSGMSRFRVLPQGLKVKQVERDAGVYCKATNGFGLSVNTLVLDISPGEKSLG 126

88 TV-----IIGELYLIKIDASPRDSGLYACTAIRTLDSPITVTVTALSSGDD--- 136

127 PDSSSGGQED--PASQOWARFRTPQSKMRRIARVGVSSVRLKCVASGHPREDITWMLK 184

137 -EDNDSESDVDNSQWRAPYVHTTKMEKRLHVAIPAANTVKKRCPAMGNPTPTMKMLK 195

185 DDQALT--PPEAEPKPKKWTLSLKNLRPDSGKYTCRVSNRGAIPNATYKVVIGIOTR 241

196 NGKEFEQEHRIIGYKVNQHMSLIMESVPSDKNTYCTIENQGSINHTYHLDVERSP 255

242 SKPLVLTGHVNTVVDGCTTSFOCKRSDVKPYIQLKRYE-----YGAEG-----R 289

256 HRLPQAGLPAANASAVVGVGEFECKYSDAOPHIQWIKIKVERNGSKYCPDGLPYQLVK 315

290 HNSTIDVGQKFFVLPFGDWSRPDGSYLK 320

316 HSG---INSSNAEVLTIYNTVTEADAGETICK 343

RESULT 7

B54846

fibroblast growth factor receptor b precursor - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 21-Jul-1995 #sequence\_revision 28-Jul-1995 #text\_change 16-Jul-1999

C:Accession: B54846

R:Takegi, Y.; Shrivastav, S.; Miki, T.; Sakaguchi, K.

J. Biol. Chem. 269, 23743-23749, 1994

A:Title: Molecular cloning and expression of the acidic fibroblast growth factor receptor

ility and covalent attachment of heparan sulfate glycosaminoglycan to the receptors.

A:Reference number: A58466; MUID:94375464

A:Accession: B54846

A>Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-822 <TAK>

C:Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; protein kinase

C:Keywords: ATP; growth factor receptor

F:172-233/Domain: immunoglobulin homology <IMM>

F:480-765/Domain: protein kinase homology <KIN>

F:488-496/Region: protein kinase ATP-binding motif

Query Match 21.6%; Score 384.5; DB 2; Length 822;

Best Local Similarity 30.2%; Pred. No. 8.8e-20;

Matches 97; Conservative 54; Mismatches 133; Indels 37; Gaps 9;

23 PPEAPORWRTWMSHGRWPCPHCAAVVEG-----DPEPLTMTKDGRTTHSGMSR 75

35 PPEPPTKYQI-----SQPEACVAPAGSELKRLMKAOAIVSWTKDG--VHLGPNR 84

76 RVL--PQGLKVKQVERDAGVYCKATNGFGLSVNTLVLDISPGEKSLGPDSSGGQ 134

85 TVLIGELYLIKIDASPRDSGLYACTAIRTLDSPITVTVTALSSGDDDDTDTSDVF 144

135 EDPASQOWARFRTPQSKMRRIARVGVSSVRLKCVASGHPREDITWMLKDDALT---R 191

145 SENNSNORA-PYMTNTEKMEKRLHVAIPAANTVKKRCPAMGNPTPTMKMLKGEKQEH 203

192 PPEAEPKPKKWTLSLKNLRPDSGKYTCRVSNRGAIPNATYKVVIGIOTRSPKPLTGH 251

204 IGGYKVNQHMSLIMESVPSDKNTYCTIENQGSINHTYHLDVERSPHRLPQAGLP 263

252 VNTVVDGCTTSFOCKRSDVKPYIQLKRYE-----YGAEG-----RHNSTIDVGQ 299

264 AMASTVVGGEVFECKYSDAOPHIQWIKIKVERNGSKYCPDGLPYQLVKHSG---INSS 320

300 KFFVLPFGDWSRPDGSYLK 320

321 NAEVLALFNTVTEADAGETICK 341

RESULT 8

S38579

fibroblast growth factor receptor 3 - Iberian ribbed newt (fragment)

C:Species: Pleurodeles waltlil (Iberian ribbed newt)

C>Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 16-Jul-1999

C:Accession: S38579

R:Shi, D.L.; Fromentoux, V.; Launay, C.; Umhauer, M.; Boucaut, J. C.

submitted to the EMBL Data Library, November 1993

A:Description: Expression of FGFR-3 in amphibian embryos.

A:Reference number: S38579

A:Accession: S38579

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-797 <SHI>

C:Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; protein kinase

C:Keywords: ATP; growth factor receptor

F:258-331/Domain: immunoglobulin homology <IMM>

F:456-741/Domain: protein kinase homology <KIN>

F:464-472/Region: protein kinase ATP-binding motif

Query Match 21.6%; Score 384; DB 2; Length 797;

Best Local Similarity 33.8%; Pred. No. 9.2e-20;

Matches 90; Conservative 41; Mismatches 87; Indels 48; Gaps 7;

60 MWTKDGRTI-----HSGMSRFRVLPQGLKVKQVERDAGVYCKATNGFGLSVNTLV 113

67 VMKKDGISVDPPTWMSHG-----QKLKIIVSYDSDGVSCKAROSSEYLR-NVTVR 118

114 VLDISPGEKSLGPDSSGGQEDPASQOWARFRTPQSKMRRIARVGVSSVRLKCVAS 173

119 VTD-----SPSSGDEDDDESESANAPFTPTPEWMEKKLILAVPAANTVRFRCPA 169

174 GHPRPDITWMLKDDALT---PPEAEPKPKKWTLSLKNLRPDSGKYTCRVSNRGAIPN 230

170 GATPPTITWMLKGEKQEHRIIGYKVNQHMSLIMESVPSDKNTYCTIENQGSINHTY 229

231 TYKVDVIGIOTRSPKPLTGHVNTVVDGCTTSFOCKRSDVKPYIQLKRYEYGAEGRH 290

230 TYTLDVLEHTPHRLPQAGLPAANASAVVGVGEFECKYSDAOPHIQWIKIKVERNG 282

291 NSTIDVGQKFFVLPFGDWSRPDGS 316

283 -----VNGSKF-----GPDGN 293

RESULT 9

B3963

protein-tyrosine kinase (EC 2.7.1.112) cek3 precursor - chicken



C:Species: Gallus gallus (chicken)  
C:Date: 09-Nov-1990 #sequence\_revision 09-Nov-1990 #text\_change 16-Jul-1999  
C:Accession: B35963  
R:Pasquale, E.B.  
Proc. Natl. Acad. Sci. U.S.A. 87, 5812-5816, 1990  
A:Title: A distinctive family of embryonic protein-tyrosine kinase receptors.  
A:Reference number: A35963; MUID:90332672  
A:Accession: B35963  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-823 <PAS>  
A:Cross-references: GB:M35196; NID:g211444; PIDN:AAA48665.1; PID:g211445  
C:Genetics:  
A:Gene: cek3  
C:Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; prote  
C:Keywords: ATP; autophosphorylation; duplication; glycoprotein; growth factor receptor;  
F:1-22/Domain: signal sequence #status predicted <SIG>  
F:23-823/Product: protein-tyrosine kinase cek3 #status predicted <MAT>  
F:23-379/Domain: extracellular #status predicted <EXT>  
F:135-141/Region: acidic  
F:174-235/Domain: immunoglobulin homology <IM>  
F:380-400/Domain: transmembrane #status predicted <TM>  
F:401-823/Domain: intracellular #status predicted <INT>  
F:481-766/Domain: protein kinase homology <KIN>  
F:489-497/Region: protein kinase ATP-binding motif  
F:65-110,181-233,280-344/Disulfide bonds: #status predicted  
F:220,267,299,320,333/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F:519,536,628/Active site: Lys, Glu, Asp #status predicted  
F:633,646/Binding site: magnesium (Asn, Asp) #status predicted  
F:659/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted

Query Match 21.5%; Score 382; DB 2; Length 823;  
Best Local Similarity 30.8%; Pred. No. 1.3e-119;  
Matches 90; Conservative 54; Mismatches 10; Indels 48; Gaps 9;

QY 23 PPEAPQRMRTKMSHGRWPAGPHCAAVPEGDPPPL-----TWMTKDG-----R 66  
DB 38 PEEPTTKYQI-----SQPDVHSALP--GEPLERQQLKDAWMISTKKGVLGPPNR 87  
QY 67 THSGWSNFRVLPQGLKVKQYERDAGVYVCATNGFSLSVNTLVLLDISPKESLG 126  
DB 88 TV-----IIGELYDIQKDSPRDSGLYACTAIRLTDSDTLVFLVNTALSSQDD--- 136  
QY 127 PDSSSGQED--PASQOMARPRFTQPSKMRVRVAPRGSSVRLKCAVSGHPRDITMK 184  
DB 137 -EDNDSEDEPDVNDSONMRAVYHTHTDKMERRLHAVPAANTVKRCFPMGPTPTMRWLK 195  
QY 185 DDOALT--RPEAEPRKKWTLSLKNLRPDSGKYTCGRVSNRAGAINATYKVDVIOKTR 241  
DB 196 NGKEFKQDEHRIGYKVRNQHMSLIMESVPSDKNYTCIVENOGTGINHTHLDVVERSP 255  
QY 242 SKPVLGTGHPVNTVDFGGTTSFOCKVRSVDKPYIOMLKRYE-----YGAGG 288  
DB 256 HRPILQAGLRANASAVVGGDVEFYCKVYSDAOPIHQWIKHNERGSKKGPBG 307

RESULT 10  
A36477  
fibroblast growth factor receptor A2 precursor - African clawed frog  
N:Contains: fibroblast growth factor receptor A2, short splice form, protein-tyrosine k  
C:Species: Xenopus laevis (African clawed frog)  
C:Date: 08-Mar-1991 #sequence\_revision 19-Jan-1996 #text\_change 16-Jul-1999  
C:Accession: A36477; C39752  
R:Muscl, T.J.; Amaya, E.; Kirschner, M.W.  
Proc. Natl. Acad. Sci. U.S.A. 87, 8365-8369, 1990  
A:Title: Regulation of the fibroblast growth factor receptor in early Xenopus embryos.  
A:Reference number: A36477; MUID:91045998  
A:Accession: A36477  
A:Molecule type: mRNA  
A:Residues: 1-812 <MOS>  
A:Cross-references: GB:U24491; GB:M37201; NID:g857677; PIDN:AAA6868.1; PID:g857678  
A:Note: 45-Arg, 49-Thr, and 64-Ser also found

R:Frisesel, R.; David, I.B.  
Mol. Cell. Biol. 11, 2481-2488, 1991  
A:Title: cDNA cloning and developmental expression of fibroblast growth factor recept  
A:Reference number: A39752; MUID:91203867  
A:Accession: C39752  
A:Molecule type: mRNA  
A:Residues: 1-30,119-189,'G',191-418,'L',420-636,'R',638-788,'V',790-812 <FRI>  
A:Cross-references: GB:M62322; NID:g214899; PIDN:AAA4993.1; PID:g214900  
C:Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; pr  
C:Keywords: alternative splicing; ATP; autophosphorylation; duplication; glycoprotein  
protein kinase  
F:1-21/Domain: signal sequence #status predicted <SIG>  
F:22-812/Product: fibroblast growth factor receptor A2, long splice form #status pred  
F:22-372/Domain: extracellular #status predicted <EXT>  
F:22-30,119-812/Product: fibroblast growth factor receptor A2, short splice form #sta  
F:47-102/Domain: immunoglobulin homology <IM>  
F:125-132/Region: acidic  
F:167-228/Domain: immunoglobulin homology <IM2>  
F:266-339/Domain: transmembrane #status predicted <TM>  
F:373-393/Domain: immunoglobulin homology <IM3>  
F:394-812/Domain: intracellular #status predicted <INT>  
F:470-755/Domain: protein kinase homology <KIN>  
F:478-486/Region: protein kinase ATP-binding motif  
F:54-100,174-226,273-337/Disulfide bonds: #status predicted  
F:76,116,133,177,223,236,260,292,313,326/Binding site: carbohydrate (Asn) (covalent)  
F:508,525,617/Active site: Lys, Glu, Asp #status predicted  
F:622,635/Binding site: magnesium (Asn, Asp) #status predicted  
F:648/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predi

Query Match 21.4%; Score 381.5; DB 1; Length 812;  
Best Local Similarity 31.5%; Pred. No. 1.4e-19;  
Matches 95; Conservative 56; Mismatches 128; Indels 23; Gaps 10;

QY 20 RPP--PPEAPQRMRTKMSHGRWPAGPHCAAVPEGDPPPLTWMTKDGRTIHSWSRFR 76  
DB 22 RPPSTLPDEVAPKRTKEVEPYSAQPGDRITLQCRLEDDVQISN--VWKNQVQL--SETNRT 79  
QY 77 VLPQGLKVKQYERDAGVYVCATNGFSLSVNTLV-----VLLDISPKESLGPPSSSG 133  
DB 80 ITGEEIOLISNAGPDENGAYAC--VTNG--PSRTYVLCSVANSDLPAEDEDDEDDSS 135  
QY 134 QEDPASQOMA--RPFETQPSKMRVRVAPRGSSVRLKCAVSGHPRDITMKDDOALT 191  
DB 136 SEKRAEENSKRNPRLMSPREKMEKLIHAVPAKYKFCRPAKNGTPTPLRLKNNRAQO 195  
QY 192 PE---AAEPRKKWTLSLKNLRPDSGKYTCGRVSNRAGAINATYKVDVIOKTRSPVLTG 248  
DB 196 DORIGGVVRSQOTWSLIMDSVPSDKNYTCIVENKKGAINHTYQDLDVVERSPHPIQA 255  
QY 249 THPVNTVDFGGTTSFOCKVRSVDKPYIOMLKRYEYGAEGRHNSITVDGOKFV--VLEFG 307  
DB 256 GLPANTSVTGVTTAEFSCKVYSDPOPIQWLRHIEI-----NGSRVASDGPPEYELIKTA 310  
QY 308 DV 309  
DB 311 GV 312

RESULT 11  
TVHUP3  
fibroblast growth factor receptor 3 precursor - human  
N:Contains: protein-tyrosine kinase (BC 2.7.1.112)  
C:Species: Homo sapiens (man)  
C:Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 16-Jul-1999  
C:Accession: A38576; A55273; E38269; I51880  
R:Keegan, K.; Johnson, D.E.; Williams, L.T.; Hayman, M.J.  
Proc. Natl. Acad. Sci. U.S.A. 88, 1095-1099, 1991  
A:Title: Isolation of an additional member of the fibroblast growth factor receptor f  
A:Reference number: A38576; MUID:91142118  
A:Accession: A38576  
A:Molecule type: mRNA  
A:Residues: 1-806 <KEE>

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OY 246 LCTGTHVNTVDEGGTTSTQCKVRSQVYKVIQWLKRVKEGAGGRNNSIIVDGQKEV--VL 304
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 255 LQAGLEPMQATVAVLGSDVEFHCVKVYSDAQPHIQWLKHVEV-----NGSKVGPDPGIPYTVL 309

OY 305 PT 306
      |
Db 310 KT 311

RESULT 12
JC4058
fibroblast growth factor receptor-4 precursor - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 29-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 20-Jun-2000
C:Accession: JC4058
R:Shiozaki, C.; Teshitiro, K.; Asano-Miyoshi, M.; Saigo, K.; Emori, Y.; Shiohawa, K.
Gene 152, 215-219, 1995
A:Title: Cloning of cDNA and genomic DNA encoding fibroblast growth factor reee ptor--
A:Reference number: JC4058; MUID:95137391
A:Accession: JC4058
A:Molecule type: mRNA
A:Residues: 1-818 <SH1>
A:Cross-references: DDBJ:D31761; NID:G809527; PIDN:BA06539.1; PLD:G809528
C:Genetics:
A:introns: 43/1; 125/1; 158/1; 213/1; 254/1; 318/1; 364/1; 429/1; 478/1; 556/1; 619/1
C:Superfamily: Basic fibroblast growth factor receptor 1; Immunoglobulin homology; pr
C:Keywords: ATP; growth factor receptor; transmembrane protein
F:1-26/Domain: signal sequence #status predicted <SIG>
F:27-818/Product: fibroblast growth factor receptor-4 #status predicted <MAT>
F:56-110/Domain: immunoglobulin homology <IM1>
F:132-137/Domain: acidic #status predicted <AD1>
F:177-238/Domain: Immunoglobulin homology <IM2>
F:276-347/Domain: Immunoglobulin homology <IM3>
F:382-402/Domain: transmembrane #status predicted <TM1>
F:477-762/Domain: protein kinase homology <KIN>
F:485-493/Region: protein kinase ATP-binding motif

Query Match 21.2%; Score 377; DB 2; Length 818;
Best Local Similarity 32.7%; Pred. No. 3e-19;
Matches 85; Conservative 45; Mismatches 88; Indels 42; Gaps 7;

OY 76 RVLPGD-----LKVQVEREDAGVYVCATNGFGSLSVNTLVLLDDISPGEKSLGP 127
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 79 RLPLPGKIRMGVTLVLEWSDVYEDSGLYIC-VVGSGTKILRRFSISVDSLASGDEE--- 134

OY 128 DSSSGCGEDPASAQ-----QMARPRFTQPSKMRNRVYIARVGSVYLKCYASHPRPDI 180
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 135 DDEDRRDRDITADINEEPVYFFQAPYWTQPHRMKKLHAAPAGVATFKPCPAGGSPLEPTI 194

OY 181 TWMKDQDLT---PPEAAEPKRRKWTLSLKLRLPDSGSKYTCRVSNRAGAIINATYKVDVI 237

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120      133  RWLNNGKCFKGEHKLIGSLIKLKHQWMSLVMSVSPSDGNTCCVENRVSLSLYTFYDLVL 254
QY      238  QRIRSKPLVLGTGTHVNTVTVDGFTTSFQCKVRSDYKPVLIQMLKRYVYGAEGRNSTIDVG 297
      121  : : : : : | | | | | : | | | | | : | | | | | : |
Db      255  ERSSHRPLIQAQIPANTTARVSGDVEYFCVYSDAQPHIQMLKHIE-----VN 302
QY      298  GQKF-----VYLPFGDV 309
      122  | : | | | | : | | : | : |
Db      303  GSREFPDDFPYVOYLKTADI 322

RESULT 13
S16236
fibroblast growth factor receptor precursor - human
N:Alternate names: dek-related FGF receptor
N:Contains: protein-tyrosine kinase (EC 2.7.1.112)
C:Species: Homo sapiens (man)
C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 16-Jul-1999
C:Accession: S16236
C:Syno. M.: Sasaki, R.; Watanabe, T.; Ishimaru, K.; Toranishi, K.

```



```

0Y 76 RVL--POGLAKYQVBEREDQAVYVCATNGFQSLSVNTYLVYLDIISPEKESLAGEPDSSGGO 134
Db 85 TVLIGETIQTIGKAIIPRBSGLACTASTVDSSETWYEFVAVNTDAISSDD---EDDTDA 140
0Y 135 EDPASQ---QWAPRFTQPSKMRRTVITAPVGSVRLKCAVASHPREDTIMKDDOALT- 190
Db 141 EDPFVSSNNKRAEYWTNTEKMERLTAUVAANTVFKPCPAGGNPMTYMLKNGREFQ 200
0Y 191 --REBAEPRKKMYTSLKLNLRPDSQKYCYCRVSNRGAJNATYKYVDYORTSKRYVLTG 248
Db 201 EHRIGGKYVRQOHSLIMESVYBDSKKNYCYVENEYGSJNHTYHLIDVERSHPHRIIDA 260
0Y 249 THPVNTYVDEGJTSFPOCKVRSIDKPYLQWIKRYE-----YGAEG-----RHNETIDY 296
Db 261 GLPANASTVGVGDEVEFYCKVYSDAQPHIQIKHYEKNKGSYGPDGILPYLKLKHSQ---I 317
0Y 297 GGGKFFVILPCTDWSRDPDGYSLNK 320
Db 318 NSSNAEVALFENVTEADAGEYICK 341

```

**RESULT 16**

A:1794  
keratinocyte growth factor receptor precursor - human  
N:Alternate names: fibroblast growth factor receptor-related protein K-SAM  
M:Contains: protein-tyrosine kinase (EC 2.7.1.112)  
C:Species: Homo sapiens (man)  
C:Date: 31-Dec-1993 #sequence  
C:Accession: A41794; A44775  
R:Mitl, T.; Bottaro, D.P.; Fleming, T.P.; Smith, C.L.; Burgess, W.H.; Chan, A.M.; Aaronson  
Proc. Natl. Acad. Sci. U.S.A. 89, 246-250, 1992  
A:Title: Determination of ligand-binding specificity by alternative splicing: two distinct  
A:Reference number: A41794; MUID:92108030  
A:Accession: A41794  
A:Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-822 <MITR>  
A:Cross-references: GB:MB0634; MID:g186740; PID:AAA36147.1; PID:g186741  
A:Note: sequence extracted from NCBI backbone (NCBI:P:75096)  
R:Champion-Arnaud, P.; Ronstin, C.; Gilbert, E.; Gesnel, M.C.; Housaint, E.; Breathnach,  
Oncogene 6, 979-987, 1991  
A:Title: Multiple mRNAs code for proteins related to the Bcr fibroblast growth factor re  
A:Reference number: A44775; MUID:91296403  
A:Accession: A44775  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 263-362 <CHA>  
A:Cross-references: GB:S04853  
C:Keywords: ATP: autophosphorylation; duplication; g1gc>protein; growth factor receptor;  
E:1-21/Domain: signal sequence #status predicted <SIG>  
E:22-822/Product: keratinocyte growth factor receptor #status predicted <MAT>  
E:172-233/Domain: immunoglobulin homology <IMM>  
E:379-399/Domain: transmembrane #status predicted <TM>  
E:488-765/Domain: protein kinase homology <IM>  
E:52-107, 179-231, 278-340/Dissulfide bonds: #status predicted  
E:518, 335, 621/Active site: Lys, Glu, Asp #status predicted

Query Match	21.1%;	Score 375.5;	DB 2;	Length 822;
Best Local Similarity	29.9%;	Pred. No. 3.8e-19;		
Matches 97;	Conservative 55;	Mismatches 129;	Indels 43;	Gaps 10

[illegible]

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OY 135 EDPASO---QWARPPEPQSPSMRRRVARLPVGSVRLKCYASAGRPDLIMMDQALT- 190
Db 141 EDFVSENSNKRAFYWTWTEMEKRLHVAIPANTVAFRCRPGAGMPMTMKLNKGEKO 200
OY 191 --REPAERPRKKWTLSLKNLRPDSGKYTCRVSNRGAINATYKVIOIOTRSKPLVTG 248
Db 201 EHRIGGYKVRNQHMSLIMESVPSDDKNYTCVVENEGSLNHHTYHLDVRSRHPRLTA 260
OY 249 THPNTIYVDFEGTISFOCKASVDYKPYIOMLKRYE-----YGAEG-----RHNSTIDV 296
Db 261 GLPNASTIVGDEFEFCYKVSDAOPIHOMIKHVEKNGSKRYGPDGLPYLTKVLKHSQ---I 317
OY 297 GGOKFVYLPDGYWSPRDSYLNK 320
Db 318 NSSNAEVLALFNVTEDADGETYCK 341

```

## RESULT 17

fibroblast growth factor receptor 4B precursor - African clawed frog  
C:Species: Xenopus laevis (African clawed frog)  
C:Date: 10-Apr-1996 #sequence\_revision 24-May-1996 #text\_change 16-Jul-1999  
C:Accession: J04583  
R:Riou, J.F.; Clavilier, L.; Boucault, J.C.  
Biochem. Biophys. Res. Commun. 218, 198-204, 1996  
A:Title: Early regionalized expression of a novel Xenopus fibroblast growth factor re  
A:Reference number: J04583; MUID:96136300  
A:Accession: J04583  
A:Molecule type: mRNA  
A:Residues: 1-829 <RIO>  
A:Cross-references: EMBL:X89807  
A:Experimental source: embryo  
C:Comment: This receptor is a tyrosine kinase transmembrane protein and plays an impo  
C:Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; pr  
C:Keywords: ATP; embryo; fibroblast; growth factor; receptor; transmembrane protein  
E:1-26/Domain: signal sequence #status predicted <SIG>  
E:27-829/Product: fibroblast growth factor receptor 4B #status predicted <MAT>  
E:60-117/Domain: immunoglobulin homology <IM1>  
E:136-148/Region: acidic  
F:187-251/Domain: immunoglobulin homology <IM2>  
F:287-362/Domain: immunoglobulin homology <IM3>  
F:393-413/Domain: transmembrane #status predicted <TM>  
F:488-773/Domain: protein kinase homology <KIN>  
F:496-504/Region: protein kinase ATP-binding motif

Query Match 21.0%; Score 374; DB 2; Length 829;  
Best Local Similarity 32.7%; Pred. No. 4.9e-19;  
Matches 87; Conservative 49; Mismatches 104; Indels 26; Gaps 8;

[illegible]

RESULT 18  
TVHUF2

fibroblast growth factor receptor 2 precursor - human  
N:Alternate names: fibroblast growth factor receptor K-sam  
N:Contains: protein-tyrosine kinase (EC 2.7.1.112) bck; receptor-like protein-tyrosine kinase  
C:Species: Homo sapiens (man)  
C:Date: 31-Dec-1993 #sequence.revision 19-Jan-1996 #text.change 16-Jul-1999  
C:Accession: A42691; B42691; S11691; A36210; B44775; D44775  
R:Kato, M.; Hattori, Y.; Sasaki, H.; Tanaka, M.; Sugano, K.; Yazaki, Y.; Sugimura, T.;  
Proc. Natl. Acad. Sci. U.S.A. 89, 2960-2964, 1992  
A:Title: K-sam gene encodes secreted as well as transmembrane receptor tyrosine kinase.  
A:Reference number: A42691; MUID:92212948  
A:Accession: A42691  
A:Molecule type: mRNA  
A:Residues: 1-821 <KAT>  
A:Cross-references: GB:M87770; NID:g186779; PIDN:AAA59470.1; PID:g186780  
A:Accession: B42691  
A:Molecule type: mRNA  
A:Residues: 1-313,430-821 <KA2>  
A:Cross-references: GB:M87771; NID:g186781; PIDN:AAA59471.1; PID:g186782  
R:Donne, C.A.; Cumaley, G.; Bellot, F.; Kaplow, J.M.; Searioss, G.; Ruta, M.; Burgess,  
EMBO J. 9, 2685-2692, 1990  
A:Title: Cloning and expression of two distinct high-affinity receptors cross-reacting w  
A:Reference number: S11691; MUID:90360977  
A:Accession: S11691  
A:Molecule type: mRNA  
A:Residues: 1-821 <DIO>  
A:Cross-references: EMBL:X52832; NID:g31373; PIDN:CAA37014.1; PID:g31374  
R:Houssaint, E.; Blaquet, P.R.; Champion-Arnaud, P.; Gesnel, M.C.; Torriglia, A.; Court  
Proc. Natl. Acad. Sci. U.S.A. 87, 8180-8184, 1990  
A:Title: Related fibroblast growth factor receptor genes exist in the human genome.  
A:Reference number: A36210; MUID:91045961  
A:Accession: A36210  
A:Molecule type: mRNA  
A:Residues: 1-313,314-428,431-821 <HOU>  
A:Cross-references: GB:M55614; GB:M37715; NID:g339710; PIDN:AAA61188.1; PID:g339711  
R:Champion-Arnaud, P.; Ronstin, C.; Gilbert, E.; Gesnel, M.C.; Houssaint, E.; Breathnach,  
Oncogene 6, 979-987, 1991  
A:Title: Multiple mRNAs code for proteins related to the BEK fibroblast growth factor re  
A:Reference number: A44775; MUID:91296403  
A:Accession: B44775  
A:Molecule type: DNA  
A:Residues: 263-361 <CH2>  
A:Cross-references: GB:S40858; NID:g232799; PIDN:AAA19320.1; PID:g232800  
A:Accession: D44775  
A:Molecule type: DNA  
A:Residues: 759-821 <CHA>  
A:Cross-references: GB:S41873  
C:Comment: This receptor binds basic fibroblast growth factor and, with lower affinity,  
C:Genetics:  
A:Gene: GDB:FGFR2  
A:Cross-references: GDB:127273; OMIM:176943  
A:Map position: 10q25.3-10q26  
C:Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; prote  
C:Keywords: alternative splicing; ATP; autophosphorylation; duplication; glycoprotein; g  
protein kinase  
F:1-21/Domain: signal sequence #status predicted <SIG>  
F:22-821/Product: fibroblast growth factor receptor 2 #status predicted <MAT>  
F:132-138/Domain: extracellular #status predicted <EXT>  
F:132-138/Region: acidic  
F:172-233/Domain: immunoglobulin homology <IMM>  
F:378-398/Domain: transmembrane #status predicted <TM>  
F:399-821/Domain: intracellular #status predicted <INT>  
F:479-764/Domain: protein kinase homology <KIN>  
F:487-495/Region: protein kinase ATP-binding motif  
F:62-107,179-231,278-342/disulfide bonds: #status predicted  
F:83,123,228,241,265,297,318,331/binding site: carbohydrate (Asn) (covalent) #status pred  
F:517,534,526/Active site: Lys, Glu, Asp #status predicted  
F:631,644/binding site: magnesium (Asn, Asp) #status predicted  
F:657/binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted

```

0y 23 PPEAQRNRTRTSHQRNMGAPHCMAAAYVEG-----DPEPLMTWTDGRTHTSGNRF 75
      ||| : : : : : ||| : : : : :
Db 35 PEEPTKQI-----SQPEVYVAAPGESLEVRCLLKDAAVISMTDGL--VHLGPNR 84
      ||| : : : : : ||| : : : : :
0y 76 PVL-PQGAKVKEVEDBAGVYCAKATNGFSLSVYTLVLVLDLISPGKESLGPDSSSGQ 134
      ||| : : : : : ||| : : : : :
Db 85 TVLIEEYLQIKGATPRDSGLVACTASRTYDEFTWFMVNTDALISSGD-----EDDTGA 140
      ||| : : : : : ||| : : : : :
0y 135 EDPAQO---QWAPPEFTQPSKMRRRVIARPGSSVRLKCVASGHEPRDITWKKDQALT- 190
      ||| : : : : : ||| : : : : :
Db 141 EDFVSSENSNRKAPYWTMTKEKMERLHAVPANTVKFCRPGAGNMPFMRLKNGKEFKQ 200
      ||| : : : : : ||| : : : : :
0y 191 --RPAERPKKKKTLISKLRPEDSGKITCRVSRACAINATYVDTQRTSKPVLTG 248
      ||| : : : : : ||| : : : : :
Db 201 EHRIGYVRNQHMSLIMESVVPSSDKNGVTCVEMEGYSIMHTYHLDVERSPHRPLQA 260
      ||| : : : : : ||| : : : : :
0y 249 THPVTVTVDFGGTTSFOCKVRSDVAPFVIOWLKRV-----YGAEG 288
      ||| : : : : : ||| : : : : :
Db 261 GLPANAATVYGGDVEFCVKYISDAQPHLQWIKHVEKNSKIGPDC 305
      ||| : : : : : ||| : : : : :

RESULT 19
A39752
fibroblast growth factor receptor A1 precursor - African clawed frog
M:contains: fibroblast growth factor receptor A1, short splice form; protein-tyrosine
C:Species: Xenopus laevis (African clawed frog)
C:Date: 07-Feb-1992 #sequence_revision 19-Jan-1996 #text_change 16-Jul-1999
C:Accession: A39752, B39752
R:Riesel, R.; Dawid, I.B.
MOL. Cell. Biol. 11, 2481-2488, 1991
A>Title: cDNA cloning and developmental expression of fibroblast growth factor recept
A:Reference number: A39752; MUID:91203867
A:Accession: A39752
A:Molecule type: mRNA
A:Residues: 1-814 <FR1>
A:Cross-references: GB:M55163; NID:g214893; PIDN:AAA49990.1; PID:g214894
A:Accession: B39752
A:Molecule type: mRNA
A:Residues: 1-30,119-814 <FR2>
A:Cross-references: GB:M55163
C:Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; pr
C:Keywords: alternative splicing; ATP; autophosphorylation; duplication; glycoprotein;
protein kinase
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-814/Product: fibroblast growth factor receptor A1, long splice form #status exp
F:22-372/Domain: extracellular #status predicted <EXT>
F:22-30,119-814/Product: fibroblast growth factor receptor A1, short splice form #sta
F:47-102/Domain: immunoglobulin homology <IM1>
F:125-132/Region: acidic
F:167-228/Domain: immunoglobulin homology <IM2>
F:266-338/Domain: immunoglobulin homology <IM3>
F:373-393/Domain: transmembrane #status predicted <TM>
F:394-814/Domain: intracellular #status predicted <INT>
F:472-757/Domain: protein kinase #status predicted <KIN>
F:488-488/Region: protein kinase ATP-binding motif
F:54-100,174-226,273-337/Disulfide bonds: #status predicted
F:76,116,163,177,223,236,260,292,313,326/Binding site: carbohydrate (Asn) (covalent)
F:510,527,619/Active site: Lys, Glu, Asp #status predicted
F:623,637/Binding site: magnesium (Asp, Asp) #status predicted
F:650/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predi

Query Match 20 74: Score 368.5; DB 1; Length 814;
Best Local Similarity 29.74; Pred. No. 1.2e-18;
Matches 92: Conservative 57; Mismatches 122; Indels 39; Gaps 11;

0y 20 RPP---PEAPDRMTRTSHGRMPAGPHCAAAVPEGDPPL-----TWTKDGR 66
      ||| : : : : : ||| : : : : :
Db 22 RPPSLRPEVAKPKTTE-----VEPYSAR-----GGTVTLQCLTRADYQGISIMVKNGV 70
      ||| : : : : : ||| : : : : :
0y 67 THGWSRFLVPLQGLKQVEREDAGVYVCVCAKNGFCSLSVNTLVLLVDLISPGKESLG 126
      ||| : : : : : ||| : : : : :

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```

Db 71 QLE-TNRTIRTEGRIQISNAGPENGILACVLTIGPSGTYVLFISINY-SDAQSADDD 128
Qy 127 PDSSGGGDDPAAQOMA--RPFRTOPSKMRRTVIAAPVSSRLKCAVSGHPRDITM 184
Db 129 DDDNSSEERKASSENKRRPFWSHPEKMKELHAPAKTYKFCPCANGPSPALRMK 188
Qy 185 DDQALTRPE---AAEPRKKWTLISLKNLRPDSGKYTCRVSNRGAINATYKVIVORT 240
Db 189 NGKEF-RPDORIGYKVASQFWSLIMDSVPSDKGNITCYENKYGTLNHTYQDIVERS 247
Qy 241 RSKPVLGTHVNTVVDGCGTTSFOCKVRSYKVPYIOWLKREYGAESRHNSITDVGCK 300
Db 248 PHRPILQGLPAGLNVSVTVGSTAESCKYSDPQHILQWLRHLEI-----NGSRVASDGF 302
Qy 301 FV-VLPRTGDV 309
Db 303 YVEILKTAGV 312

RESULT 20
fibrinblast growth factor receptor bek precursor - mouse
N:Alternate names: bek transforming protein; fibrinblast growth factor receptor 2; keratin
C:Species: Mus musculus (house mouse)
C>Date: 30-Jun-1991 #sequence_revision 13-Mar-1997 #text_change 16-Jul-1999
R:Musnukhani, A.; Dell'Era, P.; Moscattelli, D.; Kornbluth, S.; Hanafusa, H.; Basillio, C.
Proc. Natl. Acad. Sci. U.S.A. 89, 3305-3309, 1992
A:Title: Characterization of the murine BEK fibrinblast growth factor (bFGF) receptor: act
A:Reference number: A44142; MUID:92228773
A:Accession: A44142
A>Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A:Molecule type: mRNA
A:Residues: 1-821 <MAN>
R:Kornbluth, S.; Paulson, K.E.; Hanafusa, H.
Mol. Cell. Biol. 8, 5541-5544, 1988
A:Title: Novel tyrosine kinase identified by phosphotyrosine antibody screening of cDNA
A:Reference number: A31378; MUID:89219016
A:Accession: A31378
A:Molecule type: mRNA
A:Residues: 477-821 <KOR>
A:Cross-references: GB:M23362; NID:9533219; PIDN:AAA37285.1; PID:9533220
C:Gene: bek
C:Superfamily: basic fibrinblast growth factor receptor 1; immunoglobulin homology; prote
C:Keywords: AMP; autophosphorylation; duplication; glycoprotein; growth factor receptor;
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-821/Product: immunoglobulin growth factor receptor bek #status predicted <MAT>
F:112-233/Domain: immunoglobulin homology <IMM>
F:318-398/Domain: transmembrane #status predicted <TM>
F:479-764/Domain: protein kinase homology <KIN>
F:487-495/Region: protein kinase ATP-binding motif
F:83-107-179-231-278-342/disulfide bonds: #status predicted
F:83,123,147,241,265,297,318,331/Binding site: carbohydrate (Asn) (covalent) #status pre
F:517,534,626/Active site: Lys, Glu, Asp #status predicted
F:557/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicte

```

```

Db 145 SENSNORA-PYWTTEKMKRLHACPAANTVTKRCPGAGPSTMTMLKNGKEKOEHR 203
Qy 192 PEAAEPRKKWTLISLKNLRPDSGKYTCRVSNRGAINATYKVIVORTSKPVLGTGP 251
Db 204 IGGYKVRNQHWSLIMESVPSDKGNITCYENKYGTLNHTYQDIVERSPHRPILQGLP 263
Qy 252 VNTVVDGCGTTSFOCKVRSYKVPYIOWLKREYGAESRHNSITDVGCK 288
Db 264 AMASTVGGDVEYCKYSDAQPQHILQWLRHLEI-----NGSRVASDGF 305

RESULT 21
fibrinblast growth factor receptor-1, long isoform precursor - mouse
C:Species: Mus musculus (house mouse)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 16-Jul-1999
C:Accession: I49289
R:Jin, Y.; Pasumartli, K.B.; Bock, M.E.; Lytras, A.; Kardami, E.; Cattini, P.A.
J. Mol. Cell. Cardiol. 26, 1449-1459, 1994
A:Title: Cloning and expression of fibrinblast growth factor receptor-1 isoforms in th
A:Reference number: I49289; MUID:95205422
A:Accession: I49289
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-822 <RES>
A:Cross-references: EMBL:U22324; NID:g722340; PIDN:MAC52182.1; PID:g722341
C:Superfamily: basic fibrinblast growth factor receptor 1; immunoglobulin homology; pr
C:Keywords: AMP; growth factor receptor
F:270-343/Domain: immunoglobulin homology <IMM>
F:476-761/Domain: protein kinase homology <KIN>
F:484-492/Region: protein kinase ATP-binding motif

Query Match 20.5%; Score 364.5; DB 2; Length 822;
Best Local Similarity 30.6%; Pred. No. 2,3e-18;
Matches 90; Conservative 47; Mismatches 106; Indels 51; Gaps 10;

Qy 20 RPPF--PEAQRRTKTRSHGRWAPGCAAAVPE-----GDPEPLTM----- 60
Db 22 RPAFTLPEQAQW-----GVEVEESLLVHPGDLQLKCRLRDVOST 64
Qy 61 -WTKDG-RTHSGMSRFRVLPQGLKRYQVEREDAGYVCATNGFSLVNTYLVLDI 118
Db 65 NWLRDQGLVES--NRRTIRGEVEVDSIRPADSGILACTSSPSGS-DITTSVANSDA 121
Qy 119 SPKESIGPPSSSGGQEDPA-----SQQWAPRFTOPSKMRRTVIAAPVSSVRLKCVAS 173
Db 122 LPSEDDDDDDSSSEKETDNTKPNRPVAPYVTSPEKMKELHAPAKTYKFCPCSS 181
Qy 174 GHRPDTMWMKDQALTRPE---AAEPRKKWTLISLKNLRPDSGKYTCRVSNRGAIN 229
Db 182 GTRNPLRLWLNKKEF-KPDHRTIGYKVRATATSLIMDSVPSDKGNITCYENKYGSLN 240
Qy 230 ATYKVDVORTSKRPVLTGTHPVNTTVDFGTTSPFOCKVRSYKVPYIOWLKRE 283
Db 241 HTYQDIVERSPHRPILQGLPAGLNVSVTVGSTAESCKYSDPQHILQWLRHLEI 294

RESULT 22
A56182
fibrinblast growth factor receptor 2 isoform IIIB - African clawed frog (fragment)
C:Species: Xenopus laevis (African clawed frog)
C>Date: 19-Oct-1995 #sequence_revision 19-Jan-1996 #text_change 16-Jul-1999
C:Accession: A56182
R:Mathieu, M.; Kieffer, P.; Mason, I.; Dickson, C.
J. Biol. Chem. 270, 6779-6787, 1995
A:Title: Fibrinblast growth factor (bFGF) 3 from Xenopus laevis (XFGF3) binds with high
A:Reference number: A56182; MUID:95204476
A:Accession: A56182
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-480 <MAT>

```







GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: May 2, 2002, 08:50:24 ; Search time 13.22 Seconds  
(without alignments)  
893.046 Million cell updates/sec

Title: US-09-823-038A-33  
Perfect score: 1779  
Sequence: 1 RRAPCCCSCRCRCMGPSHR.....VLPTGDVMSRPDGSYLNKPL 322

Scoring table:  
BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	391	22.0	801	1	FGRI_MOUSE
2	382	21.5	823	1	CEK3_CHICK
3	381.5	21.4	812	1	FGRI_XENLA
4	378	21.2	806	1	FGRI_HUMAN
5	375.5	21.1	806	1	CEK2_CHICK
6	371.5	20.9	821	1	FGRI_HUMAN
7	366.5	20.6	802	1	FGRI_HUMAN
8	364.5	20.5	822	1	FGRI_MOUSE
9	362.5	20.4	822	1	FGRI_RAT
10	361.5	20.3	819	1	FGRI_CHICK
11	361	20.3	821	1	FGRI_MOUSE
12	360.5	20.3	822	1	FGRI_HUMAN
13	358.5	20.2	808	1	FGRI_MOUSE
14	354.5	18.8	813	1	FGRI_XENLA
15	307	17.3	654	1	BFR2_HUMAN
16	254	14.3	2029	1	LAR_DROME
17	243.5	13.7	1052	1	FGRI_MOUSE
18	225	12.6	1302	1	NRG_DROME
19	224	12.6	3707	1	PGBM_MOUSE
20	222.5	12.5	4393	1	PGBM_HUMAN
21	219.5	12.3	730	1	FGRI_HUMAN
22	208	11.7	1040	1	EGIS_CAEEL
23	207	11.6	1447	1	DCC_HUMAN
24	207	11.6	1447	1	DCC_MOUSE
25	202.5	11.4	1040	1	AXOI_RAT
26	201.5	11.3	1020	1	CONT_MOUSE
27	201.5	11.3	1912	1	PTPD_HUMAN
28	200	11.2	2012	1	DSCA_HUMAN
29	199.5	11.2	853	1	NCAL_BOVIN
30	198.5	11.2	1914	1	KMLS_HUMAN
31	197.5	11.1	1018	1	CONT_HUMAN
32	193.5	10.9	1040	1	AXOI_HUMAN
33	193.5	10.9	1906	1	KMLS_CHICK

34	192.5	10.8	1010	1	CONT_CHICK	p14781 gallus gall
35	191.5	10.8	1897	1	PTPE_HUMAN	p10586 homo sapien
36	191	10.7	1091	1	NCAL_CHICK	p13580 gallus gall
37	190.5	10.7	838	1	NCAL_RAT	p13596 rattus norv
38	190.5	10.7	1051	1	PTK7_CHICK	q91048 gallus gall
39	190	10.7	761	1	NCAL2_HUMAN	p13592 homo sapien
40	190	10.7	848	1	NCAL_HUMAN	p13591 homo sapien
41	190	10.7	898	1	FAS2_SCHAM	p22648 schistocerc
42	185.5	10.4	1070	1	PTK7_HUMAN	q13308 homo sapien
43	182.5	10.3	725	1	NCAL2_MOUSE	p13594 mus musculu
44	182.5	10.3	1115	1	NCAL_MOUSE	p13595 mus musculu
45	180	10.1	1036	1	AXOI_CHICK	p28685 gallus gall
46	180	10.1	1284	1	NRCA_CHICK	p35331 gallus gall
47	174	9.8	811	1	FS22_DROME	p34083 dtrosophila
48	174	9.8	873	1	FS21_DROME	p34082 dtrosophila
49	168	9.4	837	1	NCM2_MOUSE	q35136 mus musculu
50	165.5	9.3	837	1	NCM2_HUMAN	p13594 mus musculu
51	165.5	9.3	1257	1	CAML_HUMAN	q15394 homo sapien
52	163.5	9.2	338	1	LAMP_HUMAN	p32004 homo sapien
53	163.5	9.2	1493	1	NEOI_MOUSE	q13449 homo sapien
54	162.5	9.1	1259	1	CAML_MOUSE	p97798 mus musculu
55	162	9.1	1461	1	NEOI_RAT	q05695 rattus norv
56	161.5	9.1	521	1	BGPI_MOUSE	q92859 homo sapien
57	161.5	9.1	1260	1	CAML_MOUSE	p31809 mus musculu
58	160.5	9.0	338	1	LAMP_RAT	p11627 mus musculu
59	160.5	9.0	1142	1	MYPE_RAT	q62813 rattus norv
60	158.5	8.9	359	1	LACH_DROME	q24372 homo sapien
61	158.5	8.9	1092	1	NCAL2_XENLA	q24372 dtrosophila
62	158.5	8.9	1333	1	VGRI_MOUSE	p36335 xenopus lae
63	157	8.8	1356	1	VGRI_HUMAN	p35969 mus musculu
64	157	8.8	1377	1	NEOI_RAT	p35968 homo sapien
65	156.5	8.8	1465	1	MYM2_HUMAN	p97603 rattus norv
66	156	8.8	1266	1	NCAL_CHICK	p54296 homo sapien
67	155.5	8.7	1088	1	NCAL_XENLA	q03696 gallus gall
68	155.5	8.7	1363	1	VGRI_MOUSE	p16170 xenopus lae
69	154.5	8.7	1176	1	LAMP_CHICK	q98919 gallus gall
70	154.5	8.7	1176	1	KMLS_BOVIN	q28824 bos taurus
71	154.5	8.7	1336	1	VGRI_RAT	p53767 rattus norv
72	154	8.7	1147	1	KMLS_RABIT	p29294 oryctolagus
73	152.5	8.6	349	1	LACH_SCHAM	q26474 schistocerc
74	152.5	8.6	626	1	MAG_HUMAN	p20916 homo sapien
75	151	8.5	626	1	MAG_MOUSE	p20917 mus musculu
76	149	8.4	1443	1	NEOI_CHICK	q90610 gallus gall
77	148.5	8.3	626	1	MAG_RAT	p07722 rattus norv
78	146	8.2	333	1	AMAL_DROME	p15366 dtrosophila
79	145.5	8.2	1338	1	VGRI_HUMAN	p17948 homo sapien
80	145.5	8.2	1367	1	VGRI_MOUSE	p35918 mus musculu
81	144.5	8.1	2481	1	UN52_CAEEL	q06561 caenorhabd
82	144	8.1	537	1	MYPH_CHICK	q05693 gallus gall
83	144	8.1	739	1	VCAL_RAT	p29534 rattus norv
84	142.5	8.0	243	1	CAVT_BRALA	p05548 btanchiosteo
85	142.5	8.0	620	1	SMP_COTUA	q92134 coturnix co
86	142	8.0	353	1	CEPU_CHICK	q00773 gallus gall
87	141.5	8.0	1141	1	MYPS_HUMAN	q00872 homo sapien
88	140.5	7.9	975	1	KKIT_MOUSE	p05533 mus musculu
89	139	7.8	344	1	NTRI_RAT	q62718 rattus norv
90	139	7.8	1271	1	MYPC_CHICK	q90688 gallus gall
91	138.5	7.8	519	1	ECTO_RAT	p16573 rattus norv
92	138	7.8	621	1	MYPS_RAT	q63518 rattus norv
93	137	7.7	739	1	VCAL_MOUSE	p29535 mus musculu
94	136.5	7.7	1131	1	MYPE_CHICK	p16419 gallus gall
95	136.5	7.7	1298	1	RAGE_HUMAN	p35916 homo sapien
96	136	7.6	402	1	RAGE_RAT	q63495 rattus norv
97	135.5	7.6	978	1	KKIT_CAVHI	q28317 capra hircu
98	135.5	7.6	1343	1	MGF2_RAT	q08775 rattus norv
99	134.5	7.6	1450	1	MYSF_CHICK	q02173 gallus gall
100	134	7.5	484	1	MYPH_RAT	q08559 rattus norv

ALIGNMENTS

RESULT 1

FGF3\_MOUSE  
ID FGF3\_MOUSE STANDARD: PRT: 801 AA.  
AC 061851: 063834:  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 20-AUG-2001 (Rel. 40, Last annotation update)  
DE FIBROBLAST GROWTH FACTOR RECEPTOR 3 PRECURSOR (EC 2.7.1.112) (FGFR-3)  
GN (HEPARIN-BINDING GROWTH FACTOR RECEPTOR).  
OS FGF3 OR MFR3 OR SAM3.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA MEDLINE=92355591; PubMed=1379594;  
RT Ornitz D.M., Leder P.;  
RT "Ligand specificity and heparin dependence of fibroblast growth  
RT factor receptors 1 and 3.";  
RL J. Biol. Chem. 267:16305-16311(1992).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RX MEDLINE=93177694; PubMed=8382556;  
RA Katon O., Hattori Y., Sasaki H., Sakamoto H., Fujimoto K.,  
RA Fujii T., Sugimura T., Terada M.;  
RT "Isolation of the complementary DNA encoding a mouse heparin-binding  
RT growth factor receptor with the use of a unique kinase insert  
RT sequence.";  
RT Cancer Res. 53:1136-1141(1993).  
CC -1- FUNCTION: RECEPTOR FOR ACIDIC AND BASIC FIBROBLAST GROWTH  
CC FACTORS. PREFERENTIALLY BINDS ACIDIC FGF.  
CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP + PROTEIN  
CC TYROSINE PHOSPHATE.  
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
CC SKIN, HEAD AND LIVER BUT NOT IN MUSCLE. IN ADULT, HIGHEST LEVELS  
CC IN BRAIN. ALSO EXPRESSED IN LIVER, LUNG, KIDNEY, TESTIS, OVARY  
CC AND UTERUS. VERY LOW LEVELS IN HEART, THYMUS, SPLEEN AND MUSCLE.  
CC -1- DEVELOPMENTAL STAGE: EXPRESSED IN EMBRYO FROM MID-GESTATION AND  
CC IN ADULT.  
CC -1- SIMILARITY: BELONGS TO THE FIBROBLAST GROWTH FACTOR RECEPTOR  
CC FAMILY  
CC -1- SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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CC -----  
DR EMBL: M81342; AAA39535.1; -  
DR EMBL: S56291; AAB25535.1; -  
DR HSSP: P11362; 1FGL.  
DR MGD: MGI:95524; Fgfr3.  
DR InterPro: IPR000719; Euk\_pkinase.  
DR InterPro: IPR003006; Ig\_MHC.  
DR InterPro: IPR003598; Ig\_C2.  
DR InterPro: IPR001245; Tyr\_kin.  
DR Pfam: PF00047; Ig\_3.  
DR Pfam: PF00069; pkinase; 1.  
DR PRINTS: PR00109; TYRKINASE.  
DR SMART: SM00408; IGC2; 3.  
DR SMART: SM00219; Tyrc; 1.  
DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE: PS00109; PROTEIN\_KINASE\_TYR; 1.  
DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
KW Receptor; Glycoprotein; Tyrosine-protein kinase; ATP-binding;  
KW Transferase; Phosphorylation; Transmembrane; Immunoglobulin domain;  
KW Signal.  
FT SIGNAL 1 20 POTENTIAL.

FT CHAIN 21 801 FIBROBLAST GROWTH FACTOR RECEPTOR 3.  
FT DOMAIN 21 369 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 370 390 POTENTIAL.  
FT DOMAIN 391 801 CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 522 114 IG-LIKE C2-TYPE DOMAIN 1.  
FT DOMAIN 163 229 IG-LIKE C2-TYPE DOMAIN 2.  
FT DOMAIN 262 340 IG-LIKE C2-TYPE DOMAIN 3.  
FT DOMAIN 466 756 PROTEIN KINASE.  
FT NP\_BIND 472 481 ATP (BY SIMILARITY).  
FT BINDING 502 502 ATP (BY SIMILARITY).  
FT ACT\_SITE 611 611 BY SIMILARITY.  
FT MOD\_RES 642 642 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).  
FT DISULFID 59 107 POTENTIAL.  
FT DISULFID 170 222 POTENTIAL.  
FT DISULFID 269 333 POTENTIAL.  
FT CARBOHYD 96 96 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 219 219 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 256 256 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 288 288 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 309 309 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 322 322 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CONFLICT 684 684 P -> L (IN REF. 2).  
FT CONFLICT 687 687 MISSING (IN REF. 2).  
SQ SEQUENCE 801 AA; 87758 MW; 68BC110212691705 CRC64;

Query Match 22.0%; Score 391; DB 1; Length 801;  
Best Local Similarity 32.1%; Pred. No. 2,8e-22;  
Matches 102; Conservative 50; Mismatches 132; Indels 34; Gaps 9;

QY 5 CCSCRCRCWCWSPHPPPEAPQFRWRMSHGRWAPGPHCA-----AVEVEG 54  
DB 6 CVLFEVAVAGATSTSPPEGEQVRAAEVPEPEEQEOVAFSGDVELSCHPPGGA 65  
QY 55 PPELTMTDGTIRTHSGWSEFRVLPQGLKYKOVERDAGVVC--KATNGFSLSVNYTL 112  
DB 66 PPGPTWANDGGLVLS-HRIIVGPORLVLANSHDAGVSCQHRLTR---RVLCHEFSV 121  
QY 113 VVLDDISPKESIGPPSSSGGODEPASPQOMARPRFQPSKMRRTVARVGSVRKCA 172  
DB 122 RYTDASSSGDDEGEVY-----EDTGAPYV-----TRPERMDKLLAVPAANTVRRCFA 172  
QY 173 SGHPREDITWMDQALT---RPEAEPRKKWTLSLKNLRDESGKYCYRYSNRAGAIN 229  
DB 173 AGNPSPSISWLNKNGKREHRIIGIKLRHQWSLYMESVPSDRGNTCYVENKRGJSIR 232  
QY 230 AITYKVIVIRTSKPYLTGTHVNTIVDVGITTSFQCKYRSQVYQWLVKRYEIGAEGR 289  
DB 233 QYTTLDVLEERSPHRPIIAGLPAANTAIIGSDVEFCKYSDAOPRIQWLKHVEV----- 287  
QY 290 HNSTIDVGGQKPY-VLPPT 306  
DB 288 NGSKVGPDGTPYTVLYKT 305

RESULT 2  
CEK3\_CHICK  
ID CEK3\_CHICK STANDARD: PRT: 823 AA.  
AC P18461:  
DT 01-NOV-1990 (Rel. 16, Created)  
DT 01-NOV-1990 (Rel. 16, Last sequence update)  
DT 20-AUG-2001 (Rel. 40, Last annotation update)  
DE TYROSINE KINASE RECEPTOR CEK3 PRECURSOR (EC 2.7.1.112).  
GN CEK3.  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=90332672; PubMed=2165604;  
RA Pasquale E.B.;



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FT CHAIN 21 812 FIBROBLAST GROWTH FACTOR RECEPTOR 1.
FT DOMAIN 21 371 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 372 393 POTENTIAL.
FT DOMAIN 394 812 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 47 107 IG-LIKE C2-TYPE DOMAIN 1.
FT DOMAIN 167 233 IG-LIKE C2-TYPE DOMAIN 2.
FT DOMAIN 266 344 IG-LIKE C2-TYPE DOMAIN 3.
FT DOMAIN 472 761 PROTEIN KINASE.
FT NP_BIND 478 486 ATP (BY SIMILARITY).
FT BINDING 508 508 ATP (BY SIMILARITY).
FT ACT_SITE 617 617 BY SIMILARITY.
FT MOD_RES 648 648 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT CARBOHYD 76 76 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 116 116 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 133 133 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 177 177 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 223 223 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 236 236 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 260 260 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 292 292 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 313 313 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 326 326 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT SEQUENCE 812 AA; 90502 MM; B06333BAFEAC5C9B CRC64;

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Query Match 21.4%; Score 381.5; DB 1; Length 812;
Best Local Similarity 31.5%; Pred. No. 1.5e-21;
Matches 95; Conservative 56; Mismatches 128; Indels 23; Gaps 10;

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QY 20 RPP---PPEAPQRRRTWMSGRNAPGHCANAVVEDPPRLMTWTDGRTIHSGMSRRF 76
DB 22 RPPSTLDEAPAPKTEVEPYSAOPGRITLQCLREDVOSIN-VWKNQVOL-SETNRR 79
QY 77 VLPQGLKVKOVERADAGVYCKATNGFSLSVNTL---VLDDISGKSLGPDSSSG 133
DB 80 ITGEEIOLISAGBEDNCGVAC-VTNG---PSRTTYLCSVNSDALPSAEDDDDDDNSS 135
QY 134 QEDPASQOWA--RPRFTQSPKRRRTIARVGVSSVRLKCVASGHPRDITWMDQALTR 191
DB 136 SEEKAENSKRNPRLMSPHEKMEKILHAIPAATKVFRCFANGPTPTLRLKLNKRAFOQ 195
QY 192 PE---AAEPKKKWTLSLKLRLPEDSGKYTCRYSNRAGALNATYKVYIORTSKPVLTG 248
DB 196 DQRIIGYKVSQWLSLMDVSPDSKGNVYCIYENKYGALNHVYLDLVRSPPRIQA 255
QY 249 THPVNTTVDEGCTTSPQCKRSDVKRPVIOMLKRYEGAEGRHNSITIDVGOKFV-VLPTG 307
DB 256 GLPANTSVYGTAEFSCCKYSDQPHIQMLRHET-----NGSRVASDGPYVEILKTA 310
Y 308 DV 309
DB 311 GV 312

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RESULT 4
FGR3_HUMAN STANDARD; PRT; 806 AA.
ID FGR3_HUMAN P22607; Q16294; Q14308;
AC 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE FIBROBLAST GROWTH FACTOR RECEPTOR 3 PRECURSOR (EC 2.7.1.112) (FGR3-3).
GN FGR3 OR JTK4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (LONG ISOFORM).
RX MEDLINE=91142118; PubMed=1847508;
RA Keegan K., Johnson D.E., Williams L.T., Hayman M.J.;
RT "Isolation of an additional member of the fibroblast growth factor
RT receptor family, FGR3-3."

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RL Proc. Natl. Acad. Sci. U.S.A. 88:1095-1099(1991).
RN [2]
RP SEQUENCE FROM N.A. (SHORT ISOFORM).
RA Terada M., Shimizu A., Seo M.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 76-806 FROM N.A. (LONG ISOFORM), AND TISSUE SPECIFICITY.
RC TISSUE=Fetal brain;
RX MEDLINE=92147110; PubMed=1664411;
RA Thompson L.M., Plummer S., Schalling M., Altherr M.R., Gusella J.F.,
RA Housman D.E., Wasmuth J.J.;
RT "A gene encoding a fibroblast growth factor receptor isolated from the
RT Huntington disease gene region of human chromosome 4."
RN [4]
RP SEQUENCE OF 614-681 FROM N.A.
RX MEDLINE=91062389; PubMed=2247464;
RA Partanen J., Maekela T.P., Altalo R., Lehtvaesialho H.,
RA Altalo K.;
RT "Putative tyrosine kinases expressed in K-562 human leukemia cells."
RN [5]
RP Proc. Natl. Acad. Sci. U.S.A. 87:8913-8917(1990).
RN [6]
RP VARIANT ACH ARG-380.
RX MEDLINE=94359611; PubMed=8078586;
RA Rousseau F., Bonaventure J., Legault-Mallet L., Pelet A., Rozet J.-M.,
RA Marteau P., Le Merrier M., Munnich A.;
RT "Mutations in the gene encoding fibroblast growth factor receptor-3
RT in achondroplasia."
RL Nature 371:252-254(1994).
RN [6]
RP VARIANT ACH ARG-380.
RX MEDLINE=95150025; PubMed=7847369;
RA Bellus G.A., Hefferon T.W., de Luna R.I., Hecht J.T., Horton W.A.,
RA Machado M., Kaitila I., McIntosh I., Francome C.A.;
RT "Achondroplasia is defined by recurrent G380R mutations of FGR3."
RL Am. J. Hum. Genet. 56:368-373(1995).
RN [7]
RP VARIANT ACH CYS-375.
RX MEDLINE=95278277; PubMed=7758520;
RA Superti-Furga A., Eich G., Bucher H.U., Wisser J., Gledion A.,
RA Gitzelmann R., Steinmann B.;
RT "A glycine 375-to-cysteine substitution in the transmembrane domain
RT of the fibroblast growth factor receptor-3 in a newborn with
RT achondroplasia."
RL Eur. J. Pediatr. 154:215-219(1995).
RN [8]
RP VARIANT TD1 CYS-249.
RX MEDLINE=96154693; PubMed=8589699;
RA Tavorimla P.L., Rimoin D.L., Conn D.H., Zhu Y.-Z., Shiang R.,
RA Wasmuth J.J.;
RT "Another mutation that results in the substitution of an unpaired
RT cysteine residue in the extracellular domain of FGR3 in
RT thanatophoric dysplasia type I."
RL Hum. Mol. Genet. 4:2175-2177(1995).
RN [9]
RP VARIANTS TD1 CYS-248 AND CYS-371, AND VARIANT TD2 GLU-650.
RX MEDLINE=95291326; PubMed=7773297;
RA Tavorimla P.L., Shiang R., Thompson L.M., Zhu Y.-Z., Wilkin D.J.,
RA Lachman R.S., Wilcox W.R., Rimoin D.L., Conn D.H., Wasmuth J.J.;
RT "Thanatophoric dysplasia (types I and II) caused by distinct
RT mutations in fibroblast growth factor receptor 3."
RL Nat. Genet. 9:321-328(1995).
RN [10]
RP VARIANT HYPOCHONDROPLASIA IYS-540.
RX MEDLINE=95400307; PubMed=7670477;
RA Bellus G.A., McIntosh I., Smith E.A., Aylsworth A.S., Kaitila I.,
RA Horton W.A., Greenhaw G.A., Hecht J.T., Francome C.A.;
RT "A recurrent mutation in the tyrosine kinase domain of fibroblast
RT growth factor receptor 3 causes hypochondroplasia."
RL Nat. Genet. 10:357-359(1995).
RN [11]
RP VARIANT CROUZON GLU-391.
RX MEDLINE=96083601; PubMed=7493034;

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RA Meyers G.A., Orlow S.J., Munro I.R., Przylepa K.A., Jabs E.W.;  
RT "fibroblast growth factor receptor 3 (FGFR3) transmembrane mutation  
in Crouzon syndrome with acanthosis nigricans.";  
RL Nat. Genet. 11:462-464(1993).  
RN [12]  
RP CHARACTERIZATION OF VARIANT ACH ARG-380.  
RX MEDLINE-96174812; PubMed-8599935;  
RA Webster M.K., Donoghue D.J.;  
RT "constitutive activation of fibroblast growth factor receptor 3 by  
the transmembrane domain point mutation found in achondroplasia.";  
RL EMBO J. 15:520-527(1996).  
RN [13]  
RP VARIANTS TD1 CYS-248; CYS-249; CYS-370 AND CYS-373.  
RX MEDLINE-96254981; PubMed-8845844;  
RA Rousseau F., el Ghoulzi V., Delcroix A.L., Legat Mallet L.,  
RA Le Merrier M., Munnich A., Bonaventure J.;  
RT "Missense FGFR3 mutations create cysteine residues in thanatophoric  
dwarfism type I (TD1).";  
RL Hum. Mol. Genet. 5:509-512(1996).  
RN [14]  
RP VARIANT CRS3 ARG-250.  
RX MEDLINE-97195541; PubMed-9042914;  
RA Muenke M., Gripp K.W., McDonald-McGinn D.M., Gaudenz K.,  
RA Whitaker L.A., Bartlett S.P., Markowitz R.I., Robin N.H., Nwokoro N.,  
RA Mulvihill J.J., Losken H.W., Mulliken J.B., Guttmacher A.E.,  
RA Milroy R.S., Clarke L.A., Hollway G., Ades L.C., Haan E.A.,  
RA Molloy J.C., Cohen M.W., Jr., Bellus G.A., Fracconaro C.A.,  
RA Moloney D.M., Wall S.A., Wilkie A.O.M., Zackai E.H.;  
RT "A unique point mutation in the fibroblast growth factor receptor 3  
gene (FGFR3) defines a new craniosynostosis syndrome.";  
RL Am. J. Hum. Genet. 60:555-564(1997).  
RN [15]  
RP VARIANT TD1 CYS-370.  
RX MEDLINE-99004917; PubMed-9790257;  
RA Katsumata N., Kuno T., Miyazaki S., Mikami S., Nagashima-Miyokawa A.,  
RA Nishimura A., Horikawa R., Tanaka T.;  
RT "G370C mutation in the FGFR3 gene in a Japanese patient with  
thanatophoric dysplasia.";  
RL Endocr. J. 45:5171-5174(1998).  
RN [16]  
RP VARIANT HYPOCHONDROPLASIA VAL-538.  
RX Gigelioniene G., Hagenaes L., Ekloef O., Neumeier L., Haereld P.E.,  
RA Anvret M.;  
RT "A novel missense mutation Ile538Val in the fibroblast growth  
factor receptor 3 in hypochondroplasia.";  
RL Hum. Mutat. 11:333-333(1998).  
RN [17]  
RP VARIANT HYPOCHONDROPLASIA THR-540.  
RX MEDLINE-98112422; PubMed-9452043;  
RA Deutz-Tellouw P.P., Losekoot M., Aalfs C.M., Hennekam R.C.M.,  
RA Bakker E.;  
RT "Asn540Thr substitution in the fibroblast growth factor receptor 3  
tyrosine kinase domain causing hypochondroplasia.";  
RL Hum. Mutat. Suppl. 1:562-565(1998).  
RN [18]  
RP VARIANT TD1 MET-650.  
RA Kitch H., Brodie S.G., Kupke K.G., Lachman R.S., Wilcox W.R.;  
RT "Lys650Met substitution in the tyrosine kinase domain of the  
fibroblast growth factor receptor gene causes thanatophoric dysplasia  
type I.";  
RL Hum. Mutat. 12:362-363(1998).  
CC -1- FUNCTION: RECEPTOR FOR ACIDIC AND BASIC FIBROBLAST GROWTH  
CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP + PROTEIN  
CC -1- TYROSINE PHOSPHATE.  
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: A LONG FORM (SHOWN HERE) AND A  
CC SHORT FORM: ARE PRODUCED BY ALTERNATIVE SPLICING.  
CC -1- TISSUE SPECIFICITY: EXPRESSED IN BRAIN, KIDNEY AND TESTIS. VERY  
CC LOW OR NO EXPRESSION IN SPLEEN, HEART, AND MUSCLE. IN 20-TO 22-  
CC WEEK OLD FETUSES IT IS EXPRESSED AT HIGH LEVEL IN KIDNEY, LUNG,  
CC SMALL INTESTINE AND BRAIN, AND TO A LOWER DEGREE IN SPLEEN, LIVER,  
CC AND MUSCLE.

CC -1- DISEASE: DEFECTS IN FGFR3 ARE THE CAUSE OF THE AUTOSOMAL  
CC DOMINANT DISEASE ACHONDROPLASIA (ACH). THE MOST FREQUENT FORM OF  
CC SHORT-LIMB DWARFISM. ACH IS CHARACTERIZED BY A LONG, NARROW TRUNK,  
CC SHORT EXTREMITIES, PARTICULARLY IN THE PROXIMAL (RHIZOMELIC)  
CC SEGMENTS, A LARGE HEAD WITH FRONTAL BOWING, HYPOPLASIA OF THE  
CC MIDFACE AND A TRIDENT CONFIGURATION OF THE HANDS.  
CC -1- DISEASE: DEFECTS IN FGFR3 ARE A CAUSE OF CROUZON SYNDROME, ALSO  
CC CALLED CRANIOFACIAL DYSOSTOSIS TYPE I (CPFI). CHARACTERIZED BY  
CC CRANIOSYNOSTOSIS (PREMATURE FUSION OF THE SKULL SUTURES),  
CC HYPERTELORISM, EXOPHTHALMOS AND EXTERNAL STRABISMUS, PARROT-BEAKED  
CC NOSE, SHORT UPPER LIP, HYPOPLASTIC MAXILLA, AND A RELATIVE  
CC MANDIBULAR PROGNATHISM.  
CC -1- DISEASE: DEFECTS IN FGFR3 ARE A CAUSE OF THANATOPHORIC DYSPLASIA  
CC (TD) (ALSO KNOWN AS THANATOPHORIC DWARFISM). THE MOST COMMON  
CC NEONATAL LETHAL SKELETAL DYSPLASIA, AFFECTED INDIVIDUALS DISPLAY  
CC FEATURES SIMILAR TO THOSE SEEN IN HOMOZYGOUS ACHONDROPLASIA. IT  
CC CAUSES SEVERE SHORENING OF THE LIMBS WITH MACROCEPHALY, NARROW  
CC THORAX AND SHORT RIBS. IN THE MOST COMMON SUBTYPE (TD1), FEMUR ARE  
CC CURVED, WHILE IN TD2, STRAIGHT FEMURS ARE ASSOCIATED WITH  
CC CLOVERLEAF SKULL.  
CC -1- DISEASE: DEFECTS IN FGFR3 ARE A CAUSE OF CRANIOSYNOSTOSIS ADELAIDE  
CC TYPE (CRS3), A FORM OF CORONAL SYNOSTOSIS (CS) CHARACTERIZED BY  
CC CRANIOSYNOSTOSIS, MIDFACE HYPOPLASIA, DOWNSLANDING PALPEBRAL  
CC FISSURES, PTOSIS, HIGHLY ARCHED PALATE, MID-TO-MODERATE  
CC SENSORINEURAL HEARING LOSS, NORMAL STATURE, BRADYDACTYLY, BROAD  
CC BIG TOES, RADIOLOGICALLY, HANDS AND FEET SHOW THIMBLE-LIKE MIDDLE  
CC PHALANGES, CONED EPIPHYSES, AND CARPAL AND TARSAL FUSIONS.  
CC -1- DISEASE: DEFECTS IN FGFR3 ARE A CAUSE OF THE AUTOSOMAL DOMINANT  
CC DISEASE HYPOCHONDROPLASIA CHARACTERIZED BY DISPROPORTIONATE SHORT  
CC STATURE. IT RESEMBLES ACHONDROPLASIA, BUT WITH A LESS SEVERE  
CC PHENOTYPE.  
CC -1- SIMILARITY: BELONGS TO THE FIBROBLAST GROWTH FACTOR RECEPTOR  
CC FAMILY.  
CC -1- SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.  
CC CC THIS SWISS-PROT ENTRY IS COPYRIGHT. IT IS PRODUCED THROUGH A COLLABORATION  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC  
Query Match 21.2%; Score 378; DB 1; Length 806;  
Best Local Similarity 31.8%; Pred. No. 2,7e-21;  
Matches 96; Conservative 54; Mismatches 118; Indels 34; Gaps 10;  
OY 16 GSHRPPPEAPQRMRWTSRMPAGPCAAYVEGDPP---PL--TMTKDGRTIHS 70  
DB 33 GRAEVEPEPEQDEQLVFGSG-----DAVELSCPPEGGMGPTVWVKDGTGLV 83  
OY 71 GWSRFVLPGLKVKQVEREDAGYVC--KATNGFSLSVNTLVLDISPKEISLDP 128  
DB 84 S-ERVLVGPRLQVLAHSHEDSGAIVSCRLTQ--RVLCFHSVYVTDAPSGDEDED 139  
OY 129 SSSGGQEDPAAQOMARPRFTQPSKRRKRVITARPVSSVRLCVASGHRPRTIMKKDOA 188  
DB 140 EAEDTGVLTGAPYV---TPRRMDKRLVLPANVTFRCPAAGNPSPISWIKNRE 194  
OY 189 LT---RPEAAPRRKKWTLSKNLRPEDSGKYTCVSRACINATYVDIORTSRSPV 245  
DB 195 FRGHRIGICIRLRQOMSLVSVSPDRGNTTVEYKKGESIRPTTLDLERSPHRPI 254  
OY 246 LTGTHPVVTYVDFGTTSPQKVRSDVRYVIOMLKRVYGAEGRINSTDVGOKFV-VL 304  
DB 255 LQAGLPANQAVLSDVFEHCKYVSDAQPHIOWLKHYEV-----NGSKVPGDGTGYVVL 309  
OY 305 PT 306  
DB 310 KT 311  
RESULT 5  
CEK2\_CHICK STANDARD; PRT; 806 AA.  
ID CEK2\_CHICK P18460;  
DT 01-NOV-1990 (Rel. 16, Created)  
DT 01-NOV-1990 (Rel. 16, Last sequence update)

[illegible]

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SQ      SEQUENCE      806 AA;  89730 MW;  B38B3C6D5F2314B6 CRC64;
Query Match      21.1%; Score 375.5; DB 1; Length 806;
Best Local Similarity 34.7%; Pred. No. 4,2e-21;
Matches 84; Conservative 44; Mismatches 95; Indels 19; Gaps 5;

OY      61 WTKDGRTHSGMRFRLVDGLKVKQVKEHEDAGYVVCATKATNFGSLSVNYTLVLDDISP 120
      1 | | | | | : : : | : : : | : : | : : | : : | : : | : : | : : | : : |
DB      72 WKRDGIGLAP--NRTHIGKLLKLTINWSDYDGLISCKPRHSNEYLG--NFYRVTD---- 125
OY      121 GRESLAPDSSSGOEDDPASQOMARPREFTOPSKMRRIARIPYGSVRYLKCVAAGHPRPDI 180
      1 | : : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : |
DB      126 -----SPSSGDEDDDEDEDEDTGVPEFWRPDKMEKKLLAVPAANTYRFGCPAGNPTPTI 180
OY      181 TWMKDQALIT---REPAAEPKKKWTLSLKNIREDPSGKYTGTRVSNRACAINATYTKVDYI 237
      1 | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : |
DB      181 VYLNKNGKEFKGHRIGGKILRHQMSLVMSVSPDRGNYTCVVENKYGNINHTYOLDVL 240
OY      238 QRTSRKPVLTGTHPVNTYTDVFGTTSFOCVKSDVDPKPVYOMLKRVE----YGAGSRHNS 292
      1 | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : |
DB      241 EKSPIRPIIQAQLPANAQYVYVSSNVEFHCXYSDAQPHIQLKHYEVNCSKIGPDPETPIV 300
OY      293 TT 294
      1 :
DB      301 FV 302

RESULT      6
FGR2_HUMAN
ID      FGR2_HUMAN      STANDARD;      PRT;      821 AA.
AC      P21802; P18443;
DT      01-NOV-1990 (Rel. 16, Created)
DI      01-JUN-1994 (Rel. 29, Last sequence update)
DR      20-AUG-2001 (Rel. 40, Last annotation update)
DE      FIBROBLAST GROWTH FACTOR RECEPTOR 2 PRECURSOR (EC 2.7.1.112) (RGFR-2)
DE      (KERATINOCYTE GROWTH FACTOR RECEPTOR).
GN      FGR2 OR BEK OR BFR-1 OR KSAM-1.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Neonatal brain stem;
RC      MEDLINE=90360977; PubMed=1697263;
RA      Dionne C.A., Crumley G.R., Bellot F., Kaplow J.M., Seartoss G.,
RA      Ruta M., Burgess W.H., Jaye M., Schlessinger J.,
RT      "Cloning and expression of two distinct high-affinity receptors
RT      cross-reacting with acidic and basic fibroblast growth factors.";
RL      EMBO J. 9;2:685-2692(1990).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      MEDLINE=91045961; PubMed=2172978;
RX      Housaint E., Bianquet P.R., Champion-Arnaud P., Gesnel M.C.,
RA      Torriglia A., Courtois Y., Breathnach R.,
RT      "Related fibroblast growth factor receptor genes exist in the human
RT      genome.";
RL      Proc. Natl. Acad. Sci. U.S.A. 87;8:180-8184(1990).
RN      [3]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Stomach cancer;
RC      MEDLINE=90332706; PubMed=2377625;
RA      Hattori Y., Odagiri H., Nakatani H., Miyagawa K., Naito K.,
RA      Sakamoto H., Katoh O., Yoshida T., Sugimura T., Terada M.,
RT      "K-sam, an amplified gene in stomach cancer, is a member of the
RT      heparin-binding growth factor receptor genes.";

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RL Proc. Natl. Acad. Sci. U.S.A. 87:5983-5987(1990).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-92212948; PubMed-1313574;  
 RA Kato M., Hattori Y., Sasaki H., Tanaka M., Sugano K., Yazaki Y.,  
 RA Sugimura T., Terada M.;  
 RT "K-sam gene encodes secreted as well as transmembrane receptor  
 RT tyrosine kinase.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 89:2960-2964(1992).  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Placenta;  
 RX MEDLINE-93016048; PubMed-1400433;  
 RA Dell K.R., Williams L.T.;  
 RT "A novel form of fibroblast growth factor receptor 2. Alternative  
 RT splicing of the third immunoglobulin-like domain confers ligand  
 RT binding specificity.";  
 RL J. Biol. Chem. 267:21225-21229(1992).  
 RN [7]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Blood;  
 RA Steinberger D., Mueller U.;  
 RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.  
 RN [8]  
 RP VARIANTS CS HIS-340; ARG-342; SER-342; TYR-342 AND CYS-354.  
 RX MEDLINE-95078932; PubMed-7987400;  
 RA Reardon W., Winter R.M., Rutland P., Pulleyn L.J., Jones B.M.,  
 RA Malcolm S.;  
 RT "Mutations in the fibroblast growth factor receptor 2 gene cause  
 RT Crozon syndrome.";  
 RL Nat. Genet. 8:98-103(1994).  
 RN [9]  
 RP VARIANTS CS CYS-328 AND CYS-347, AND VARIANT JWS GLY-344.  
 RX MEDLINE-9519174; PubMed-874170;  
 RA Jabs E.W., Li X., Scott A.F., Meyers G., Chen W., Eccles M., Mao J.,  
 RA Charles L.R., Jackson C.E., Jaye M.;  
 RT "Jackson-Weiss and Crozon syndromes are allelic with mutations in  
 RT fibroblast growth factor receptor 2.";  
 RL Nat. Genet. 8:275-279(1994).  
 RN [10]  
 RP VARIANTS CS.  
 RX MEDLINE-95384152; PubMed-7655462;  
 RA Oldridge M., Wilkie A.O.M., Stanley S.F., Poole M.D., Pulleyn L.J.,  
 RA Rutland P., Hockley A.D., Wake M.J.C., Goldin J.H., Winter R.M.,  
 RA Reardon W., Malcolm S.;  
 RT "Mutations in the third immunoglobulin domain of the fibroblast growth  
 RT factor receptor-2 gene in Crozon syndrome.";  
 RL Hum. Mol. Genet. 4:1077-1082(1995).  
 RN [11]  
 RP VARIANT PS ALA-321.  
 RX MEDLINE-95235551; PubMed-7719333;  
 RA Lejeune E., Wei M.H., Bonaventure J., Munnich A., le Merrer M.,  
 RA Renier D.;  
 RT "FGFR2 mutations in Pfeiffer syndrome.";  
 RL Nat. Genet. 9:108-108(1995).  
 RN [12]  
 RP VARIANTS AS TRP-252 AND ARG-253.  
 RX MEDLINE-95235562; PubMed-7719344;  
 RA Wilkie A.O.M., Stanley S.F., Oldridge M., Poole M.D., Ashworth G.J.,  
 RA Hockley A.D., Hayward R.D., David D.J., Pulleyn L.J., Rutland P.,  
 RA Malcolm S., Winter R.M., Reardon W.;  
 RT "Apert syndrome results from localized mutations of FGFR2 and is  
 RT allelic with Crozon syndrome.";  
 RL Nat. Genet. 9:165-172(1995).  
 RN [13]  
 RP VARIANTS PS PRO-341; ARG-342 AND TYR-342.  
 RX MEDLINE-95235563; PubMed-7719345;  
 RA Rutland P., Pulleyn L.J., Reardon W., Baraister M., Hayward R.,  
 RA Jones B., Malcolm S., Winter R.M., Oldridge M., Stanley S.F.,  
 RA Poole M.D., Wilkie A.O.M.;  
 RT "Identical mutations in the FGFR2 gene cause both Pfeiffer and  
 RT Crozon syndrome phenotypes.";  
 RL Nat. Genet. 9:173-176(1995).

RN [14]  
 RP VARIANTS CS/JWS/PS.  
 RX MEDLINE-96203627; PubMed-8644708;  
 RA Meyers G.A., Day D., Goldberg R., Daentli D.L., Przybyla K.A.,  
 RA Abrams L.J., Graham J.M. Jr., Feingold M., Moeschler J.B.,  
 RA Ramsley E., Scott A.F., Jabs E.W.;  
 RT "FGFR2 exon IIIa and IIc mutations in Crozon, Jackson-Weiss, and  
 RT Pfeiffer syndromes: evidence for missense changes, insertions, and a  
 RT deletion due to alternative RNA splicing.";  
 RL Am. J. Hum. Genet. 58:491-498(1996).  
 RN [15]  
 RP VARIANTS CS CYS-105; GLU-338; CYS-351 AND ARG-384.  
 RX MEDLINE-97101656; PubMed-8946174;  
 RA Pulleyn L.J., Reardon W., Wilkes D., Rutland P., Jones B.M.,  
 RA Hayward R., Hall C.M., Brunton L., Chun N., Lammner E., Malcolm S.,  
 RA Winter R.M.;  
 RT "Spectrum of craniosynostosis phenotypes associated with novel  
 RT mutations at the fibroblast growth factor receptor 2 locus.";  
 RL Eur. J. Hum. Genet. 4:283-291(1996).  
 RN [16]  
 RP VARIANTS CS ILE-331; ASP-336--ALA-337 DUPL AND TRP-356--THR-358 DEL.  
 RX MEDLINE-97114301; PubMed-8956050;  
 RA Steinberger D., Mulliken J.B., Mueller U.;  
 RT "Crozon syndrome: previously unrecognized deletion, duplication, and  
 RT point mutation within FGFR2 gene.";  
 RL Hum. Mutat. 8:386-390(1996).  
 RN [17]  
 RP VARIANT PS CYS-290.  
 RX MEDLINE-97295073; PubMed-9150725;  
 RA Tartaglia M., Valeri S., Velardi F., di Rocco C., Battaglia P.A.;  
 RT "Trp290Cys mutation in exon IIIa of the fibroblast growth factor  
 RT receptor 2 (FGFR2) gene is associated with Pfeiffer syndrome.";  
 RL Hum. Genet. 99:602-606(1997).  
 RN [18]  
 RP VARIANT CS L-252, VARIANT AS F-252, AND VARIANT PS F-252-S-253.  
 RX MEDLINE-97156222; PubMed-9002682;  
 RA Oldridge M., Lunt P.W., Zackai E.H., McDonald-Mcginn D.M., Muenke M.,  
 RA Moloney D.M., Twigg S.R.F., Heath J.K., Howard T.D., Hoganson G.,  
 RA Gagnon D.M., Jabs E.W., Wilkie A.O.M.;  
 RT "Genotype-phenotype correlation for nucleotide substitutions in the  
 RT Ig11-Ig111 linker of FGFR2.";  
 RL Hum. Mol. Genet. 6:137-143(1997).  
 RN [19]  
 RP VARIANT CS GLU-292.  
 RX MEDLINE-97297373; PubMed-9152842;  
 RA Steinberger D., Collmann H., Schmalenberger B., Mueller U.;  
 RT "A novel mutation (a886g) in exon 5 of FGFR2 in members of a family  
 RT with Crozon phenotype and plagiocephaly.";  
 RL J. Med. Genet. 34:420-422(1997).  
 RN [20]  
 RP VARIANTS CS VAL-276; CYS-301 AND SER-314.  
 RX MEDLINE-98180879; PubMed-9521581;  
 RA Steinberger D., Vriend G., Mulliken J.B., Mueller U.;  
 RT "The mutations in FGFR2-associated craniosynostoses are clustered in  
 RT five structural elements of immunoglobulin-like domain III of the  
 RT receptor.";  
 RL Hum. Genet. 102:145-150(1998).  
 RN [21]  
 RP VARIANTS AS TRP-252 AND ARG-253.  
 RX MEDLINE-98112406; PubMed-9452027;  
 RA Tsai F.-J., Hwu W.-L., Lin S.-P., Chang J.-G., Wang T.-R., Tsai C.-H.;  
 RT "Two common mutations 934C to G and 937C to G of fibroblast growth  
 RT factor receptor 2 (FGFR2) gene in Chinese patients with Apert  
 RT syndrome.";  
 RL Hum. Mutat. Suppl. 1:S18-S19(1998).  
 RN [22]  
 RP VARIANT PS CYS-351.  
 RX MEDLINE-98358420; PubMed-9693549;  
 RA Mathijssen I.M., Vaandrager J.M., Hoogheboom A.J.,  
 RA Hesselink-Janssen A.L., van den Ouweland A.M.W.;  
 RT "Pfeiffer's syndrome resulting from an S351C mutation in the  
 RT fibroblast growth factor receptor-2 gene.";  
 RL J. Craniofac. Surg. 9:207-209(1998).

CC -1- FUNCTION: RECEPTOR FOR ACIDIC AND BASIC FIBROBLAST GROWTH  
 CC FACTORS.  
 CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP + PROTEIN  
 CC TYROSINE PHOSPHATE.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- DISEASE: DEFECTS IN FGFR4 ARE A CAUSE OF CROZON SYNDROME (CS),  
 CC ALSO CALLED CRANIOFACIAL DYSOSTOSIS TYPE I (CFDI). CHARACTERIZED  
 CC BY CRANIOSYNOSTOSIS (PREMATURE FUSION OF THE SKULL SUTURES),  
 CC HYPERTELORISM, EXOPHTHALMOS AND EXTERNAL STRABISMUS. PARROT-BEAKED  
 CC NOSE, SHORT UPPER LIP, HYPOPLASTIC MAXILLA, AND A RELATIVE  
 CC MANIBULAR PROGNATHISM.

Query Match 20.9%; Score 371.5; DB 1; Length 821;  
 Best Local Similarity 31.6%; Pred. No. 8.6e-21;  
 Matches 90; Conservative 50; Mismatches 112; Indels 33; Gaps 8;

QY 23 PPAAPQWRFRMRSHGRMPAPHCNAAPVPG-----DEPPLTMTKDGRTTHSGSRF 75  
 DB 35 PEPPTKRYQI-----SQPEVYVAAPGSLSEVRCLLNDAAVISWTKDG--VHLGPNMR 84  
 QY 76 RVL-PGLAKYQYERDAGYVVCATNGFGLSVNTLVLLDDISPGKESLGPDSGGQ 134  
 DB 85 TVLIGELYLQKATPRDSSGLYACTASTYDSEWYVWNTDIAISSGD---EDDTIGA 140  
 QY 135 EDPASQ---QWAPRFTQPSKMRRYIARPVGSSVRLKCVASGHPRDITMKDDQALT- 190  
 DB 141 EDVSESNKRRAPDYWTNTEKMEKRLHVAAPANTVKEFCPAGNPMTWMLNKGKFEKQ 200  
 QY 191 --RPEAEPKKKWTLSIKLREDSGKYCRSNAGATNATKYVDYIORTSKPLTG 248  
 DB 201 EHRIGCYKRNQHSMLMESVPSDGNATCVVENEYGSINHYHLDVVERSPHRLQA 260  
 QY 249 THPNTVDFGTTSEFCCKYRSDPKVPIQMLKFE-----YGAEG 288  
 DB 261 GLPANNSTVYGQVEYVCKYSDAQPHIQIKHVEKNGSKYGPDG 305

RESULT 7  
 ID FGFR4\_HUMAN STANDARD; PRT; 802 AA.  
 AC P22455; Q14309; 043785;  
 DT 01-AUG-1991 (Rel. 19; Created)  
 DT 20-AUG-2001 (Rel. 40; Last sequence update)  
 DT 20-AUG-2001 (Rel. 40; Last annotation update)  
 DE FIBROBLAST GROWTH FACTOR RECEPTOR 4 PRECURSOR (EC 2.7.1.112) (FGFR-4).  
 GN FGFR4 OR JTK2 OR TKF.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 OX NCBI\_Taxid=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91224085; PubMed=1709094;  
 RA Partanen J.M., Meekelae T.P., Gerola E., Korhonen J., Hiltunen H.,  
 RA Claesson-Welsh L., Allitalo K.,  
 RT "FGFR-4, a novel acidic fibroblast growth factor receptor with a  
 RT distinct expression pattern.";  
 RL EMBO J. 10:1347-1354(1991).  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Mammary gland;  
 RX MEDLINE=93194827; PubMed=7680645;  
 RA Ron D., Reich R., Chedid M., Lengel C., Cohen O.E., Chan A.M.,  
 RA Neufeld G., Miki T., Tronick S.R.;  
 RT "Fibroblast growth factor receptor 4 is a high affinity receptor for  
 RT both acidic and basic fibroblast growth factor but not for  
 RT keratinocyte growth factor.";  
 RL J. Biol. Chem. 268:5388-5394(1993).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98119018; PubMed=9457674;  
 RA Kosztzawa M., Muller U.;  
 RT "Genomic structure and complete sequence of the human FGFR4 gene.";

RL Mamm. Genome 9:131-135(1998).  
 RN [4]  
 RP SEQUENCE OF 609-676 FROM N.A.  
 RC TISSUE=Blood;  
 RX MEDLINE=91062389; PubMed=2247464;  
 RA Partanen J., Meekelae T.P., Allitalo R., Lehesjaaho H., Allitalo K.,  
 RT "Putative tyrosine kinases expressed in k-562 human leukemia cells.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 87:8913-8917(1990).  
 CC -1- FUNCTION: RECEPTOR FOR ACIDIC FIBROBLAST GROWTH FACTOR. DOES NOT  
 CC BIND TO BASIC FIBROBLAST GROWTH FACTOR. BINDS FGF19.  
 CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP + PROTEIN  
 CC TYROSINE PHOSPHATE.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- SIMILARITY: BELONGS TO THE FIBROBLAST GROWTH FACTOR RECEPTOR  
 CC FAMILY.  
 CC -1- SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.  
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 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).

CC EMBL: X57205; CAA0490.1; -  
 CC EMBL: L03840; AAB59389.1; -  
 CC EMBL: Y13901; CAA74200.1; -  
 CC EMBL: M59373; AAB63208.1; -  
 CC PIR: S15345; TVH0F4.  
 CC HSP: P11362; 1FGI.  
 CC MIM: 134935; -  
 DR InterPro: IPR003599; Ig.  
 DR InterPro: IPR003598; Ig.  
 DR InterPro: IPR003600; Ig\_Like.  
 DR InterPro: IPR002290; Ser\_thr\_kin\_actsite.  
 DR InterPro: IPR001245; Tyr\_kin.  
 DR Pfam: PF00047; Ig; 3.  
 DR Pfam: PF00069; pkinase; 1.  
 DR PRINTS: PR00109; TYRKINASE.  
 DR SMART: SM00409; Ig; 3.  
 DR SMART: SM00408; IGC2; 3.  
 DR SMART: SM00410; IG\_Like; 2.  
 DR SMART: SM00220; S\_TKc; 1.  
 DR SMART: SM00219; Tyrc; 1.  
 DR PROSITE: PS00107; PROTEIN KINASE ATP; 1.  
 DR PROSITE: PS00109; PROTEIN KINASE\_TYR; 1.  
 DR PROSITE: PS50011; PROTEIN KINASE\_DOM; 1.  
 KW Receptor; Glycoprotein; Tyrosine-protein kinase; ATP-binding;  
 KW Transferrase; Phosphorylation; Transmembrane; Immunoglobulin domain;  
 KW Signal.  
 FT CHAIN 1..24  
 FT SIGNAL 1..24  
 FT DOMAIN 25..369  
 FT TRANSMEM 370..390  
 FT DOMAIN 391..802  
 FT DOMAIN 50..108  
 FT DOMAIN 165..231  
 FT DOMAIN 264..340  
 FT DOMAIN 467..755  
 FT NP\_BIND 473..481  
 FT BINDING 503..503  
 FT ACT\_SITE 612..612  
 FT MOD\_RES 643..643  
 FT DISULFID 57..101  
 FT DISULFID 172..224  
 FT DISULFID 271..333  
 FT CARBOHYD 112..112  
 FT CARBOHYD 258  
 FT CARBOHYD 290  
 FT CARBOHYD 311  
 FT CARBOHYD 322  
 FT CONFLICT 297

POTENTIAL.  
 FIBROBLAST GROWTH FACTOR RECEPTOR 4.  
 EXTRACELLULAR (POTENTIAL).  
 POTENTIAL.  
 CYTOPLASMIC (POTENTIAL).  
 IG-LIKE C2-TYPE DOMAIN 1.  
 IG-LIKE C2-TYPE DOMAIN 2.  
 IG-LIKE C2-TYPE DOMAIN 3.  
 PROTEIN KINASE.  
 ATP (BY SIMILARITY).  
 ATP (BY SIMILARITY).  
 BY SIMILARITY.  
 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).  
 POTENTIAL.  
 POTENTIAL.  
 N-LINKED (GLCNAc...) (POTENTIAL).  
 N-LINKED (GLCNAc...) (POTENTIAL).  
 N-LINKED (GLCNAc...) (POTENTIAL).  
 N-LINKED (GLCNAc...) (POTENTIAL).  
 N-LINKED (GLCNAc...) (POTENTIAL).  
 D-> V (IN REF. 1).



SQ SEQUENCE 802 AA; 87954 MW; B22B259831BB889F CRC64;  
 Query Match 20.6%; Score 366.5; DB 1; Length 802;  
 Best Local Similarity 32.3%; Pred. No. 2e-20;  
 Matches 91; Conservative 45; Mismatches 105; Indels 41; Gaps 9;  
 61 WTKGRTTHSGMSRFRVLPQ-----LKVQVEREDACVYCKANKNGSLSY--NY 110  
 66 WYKGG-----RLAPAGRVGWRGRLEIASFLPDAARCYCLAR--GSMIVLONL 113  
 111 TLVLVDLIDISPKESLGPSSSGQEDPA---SQQWARPFPQPSKMRRIARIPGSSVR 167  
 114 TLILGDLSTSSNDEDDPRS---HRDPSNRHSYQQAQAWYWHHPQMEKKLAIVAGNTVK 169  
 168 LKCAVAGHPRPDITWMDKDAL---TRPEAAEPRKKWTLSKLRPDSGKYTCRVSRN 224  
 170 FRCPAAGNPPTIIRMLKQGAFFHGENRIGGIRLRHQSLSVMESVPSDRGTCTCIVENA 229  
 225 AGAINATYKVVIVQRTSRKPVLTGTHPVNTVDFGCTTSPOCKYRSDVKYPIQMLKRY-- 282  
 230 VGSIRYNLTLVDLEKSPRPLQAGLPAVNTAVVGSVDVELCKYVSDAQPHIQWLKHIV 289  
 283 ---EYGAEG---RHNSTIDVGGKFFVLPYGDWVSRRPGSY 317  
 290 NGSSFGADGFPYGVVLTAKTADINSSEVEVLYLRNYSAEADAGEY 331  
 RESULT 8  
 FGRL\_MOUSE STANDARD: PRT; 822 AA.  
 ID FGRL\_MOUSE P16092; 001736; 061562;  
 DT 01-APR-1990 (Rel. 14, Created)  
 DT 01-MAY-1991 (Rel. 18, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)  
 DE BASIC FIBROBLAST GROWTH FACTOR RECEPTOR 1 PRECURSOR (EC 2.7.1.112)  
 DE (FGFR-1) (BFGF-R) (MFR).  
 GN FGRL OR FLG.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID:10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Brain;  
 RX MEDLINE-90160373; PubMed-1689490;  
 RA Reid H.H., Wilks A.F., Bernard O.;  
 RT "Two forms of the basic fibroblast growth factor receptor-like mRNA  
 are expressed in the developing mouse brain."  
 RT Proc. Natl. Acad. Sci. U.S.A. 87:1596-1600(1990).  
 RL [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BALB/C; TISSUE-Brain;  
 RX MEDLINE-90265603; PubMed-2161096;  
 RA Satrian A., Avivi A., Orr-Urtreger A., Neufeld G., Lonal P.,  
 RA Givol D., Yarden Y.;  
 RT "The murine flg gene encodes a receptor for fibroblast growth  
 factor."  
 RT Oncogene 5:635-643(1990).  
 RL [3]  
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.  
 RX MEDLINE-91207411; PubMed-1708247;  
 RA Kouhara H., Kasayama S., Saito H., Matsumoto K., Sato B.;  
 RT "Expression cDNA cloning of fibroblast growth factor (FGF) receptor  
 in mouse breast cancer cells: a variant form in FGF-responsive  
 transformed cells."  
 RT Biochem. Biophys. Res. Commun. 176:31-37(1991).  
 RL [4]  
 RP SEQUENCE FROM N.A. (SHORT FORM).  
 RX MEDLINE-90272715; PubMed-2161540;  
 RA Mansukhani A., Moscatelli D., Talarico D., Levytska V., Basillio C.;  
 RT "A murine fibroblast growth factor (FGF) receptor expressed in CHO  
 cells is activated by basic FGF and Kaposi FGF."

RL Proc. Natl. Acad. Sci. U.S.A. 87:4378-4382(1990).  
 RN [5]  
 RP SEQUENCE OF 1-15 FROM N.A., AND ALTERNATIVE SPLICING.  
 RX MEDLINE-95100926; PubMed-7802632;  
 RA Harada T., Saito H., Kouhara H., Kurebayashi S., Kasayama S.,  
 RA Terakawa N., Kishimoto T., Sato B.;  
 RT "Murine fibroblast growth factor receptor 1 gene generates multiple  
 messenger RNAs containing two open reading frames via alternative  
 splicing."  
 RT Biochem. Biophys. Res. Commun. 205:1057-1063(1994).  
 RL [6]  
 RP FUNCTION: RECEPTOR FOR BASIC FIBROBLAST GROWTH FACTOR. A SHORTER  
 FORM OF THE RECEPTOR COULD BE A RECEPTOR FOR ACIDIC FGF (ARFGF).  
 CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP + PROTEIN  
 TYROSINE PHOSPHATE  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- ALTERNATIVE PRODUCTS: 3 ISOFORMS: A LONG FORM (SHOWN HERE), A  
 VARIANT FORM AND A SHORT FORM ARE PRODUCED BY ALTERNATIVE  
 SPLICING.  
 CC -1- SIMILARITY: BELONGS TO THE FIBROBLAST GROWTH FACTOR RECEPTOR  
 FAMILY.  
 CC -1- SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC EMBL: M28998; AAA37290.1; -;  
 CC EMBL: X51893; CAA36175.1; -;  
 CC EMBL: M65053; AAA37620.1; -;  
 CC EMBL: M33760; AAA37622.1; -;  
 CC EMBL: S74765; AAB32845.1; ALT\_SEQ.  
 CC PIR: A34849; TVMSFG.  
 CC HSP: P11362; IFC1.  
 CC MGI: MGI:95522; Fgfr1.  
 DR InterPro: IPR000719; Euk\_Dkinase.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003598; Ig\_C2.  
 DR InterPro: IPR001245; Tyr\_kin.  
 DR Pfam: PF00047; Ig\_3.  
 DR Pfam: PF00069; pkinase.1.  
 DR PRINTS: PR00109; TYRKINASE.  
 DR SMART: SM00408; IGC2; 3.  
 DR SMART: SM00219; TYRC; 1.  
 DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE: PS00109; PROTEIN\_KINASE\_TYR; 1.  
 DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
 KW Receptor; Glycoprotein; Tyrosine-protein kinase; ATP-binding;  
 KW Transferase; Phosphorylation; Transmembrane; Signal;  
 KW Immunoglobulin domain; Alternative splicing.  
 FT SIGNAL 1 21  
 FT CHAIN 22 822  
 FT 1  
 FT BASIC FIBROBLAST GROWTH FACTOR RECEPTOR  
 FT 1  
 FT EXTRACELLULAR (POTENTIAL).  
 FT POTENTIAL.  
 FT CYTOPLASMIC (POTENTIAL).  
 FT IG-LIKE C2-TYPE DOMAIN 1.  
 FT IG-LIKE C2-TYPE DOMAIN 2.  
 FT IG-LIKE C2-TYPE DOMAIN 3.  
 FT PROTEIN KINASE.  
 FT ATP (BY SIMILARITY).  
 FT ATP (BY SIMILARITY).  
 FT BY SIMILARITY.  
 FT PHOSPHORYLATION (AUTO-) (BY SIMILARITY).  
 FT POTENTIAL.  
 FT POTENTIAL.  
 FT POTENTIAL.  
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 117 117  
 FT CARBOHYD 227 227

FT	CARBOHYD	240	240	N-LINKED (GLCNAC. .)	(POTENTIAL).
FT	CARBOHYD	264	264	N-LINKED (GLCNAC. .)	(POTENTIAL).
FT	CARBOHYD	296	296	N-LINKED (GLCNAC. .)	(POTENTIAL).
FT	CARBOHYD	317	317	N-LINKED (GLCNAC. .)	(POTENTIAL).
FT	CARBOHYD	330	330	N-LINKED (GLCNAC. .)	(POTENTIAL).
FT	VARSPLIC	30	30	Q -> QSSSSWWVA (IN VARIANT FORM).	
FT	VARSPLIC	31	119	MISSING (IN SHORT ISOFORM).	
FT	VARSPLIC	148	149	MISSING (IN VARIANT FORM).	
FT	CONFLICT	229	229	T -> S (IN REF. 4).	
FT	CONFLICT	256	258	ILQ -> HPS (IN REF. 1 AND 3).	
FT	CONFLICT	270	270	G -> A (IN REF. 4).	
FT	CONFLICT	387	387	I -> M (IN REF. 3).	
FT	CONFLICT	440	440	G -> A (IN REF. 2).	
FT	CONFLICT	508	508	V -> L (IN REF. 4).	
FT	CONFLICT	544	544	I -> M (IN REF. 3).	
FT	CONFLICT	756	756	R -> H (IN REF. 1).	
FT	CONFLICT	765	765	E -> D (IN REF. 4).	
SO	SEQUENCE	822 AA;	91960 MW;	DS34695F680926B	CRC64;

Query Match	20.5%	Score 364.5;	DB 1	Length 822;
Best Local Similarity	30.6%	Pred. No. 2.9e-20;		
Matches	90;	Conservative	47;	Mismatches 106;
				Indels 51;
				Gaps 10

QY	20	RPPRPP--PAPQWKKRKMSHGRRWAPGHCAAVNP-----GDPPEPLTM-----	60
Db	22	RPAPLPLEDAQEW-----GVPRVESLLVHGDDLTLQLRRLDDVGS	64
QY	61	-WKAD-RTHSGWSEFRFLPQGLKVKOVEREDYGVYCATKGFSLSNVTLVLDDI	111
Db	65	NMLRDSDVOLVES--NRTRTITGHEVVRCSIPADSGIACVTSPGSS--DTTFVSNVSDA	12
QY	119	SPEKESLGPDSSSGGQEDPA-----SOOMARPTQPSKKRRRVIAAPRGSSVRLCVAS	177
Db	122	LPSEDDDDDDSSSEKEETNDTKPNRRPAPAYPTSPENKEKKLHVPAAKTYVFKRCSS	18
QY	174	GHRPDTITMKDQDLALPPE-----AAERKKKATLSLKNLRPDSKTYCYCRYSNRGAIN	22
Db	182	GTPNPLIRKLKNGKEP-KPDRIRIGYKRIATWSIIMDSVSPDKKNYTCIYENEGSIN	24
QY	230	ATYKVDVIORTSKSVYLGTHPVPNTVYDFGGTTSFOCKVRSADVKIOMLRKE	283
Db	241	HTIQDLQVVERSHRPIIADGLPAAKTYVALGSNVEWFKCYSDQPHIOMLKIE	294

	RESULT	9		
	FGFR1_RAT			
ID	FGFR1_RAT	STANDARD:	PRT;	822 AA.
AC	004589;			
DT	01-JUN-1994 (Rel. 29, Created)			
DT	01-JUN-1994 (Rel. 29, Last sequence update)			
DT	20-AUG-2001 (Rel. 40, Last annotation update)			
DE	BASIC FIBROBLAST GROWTH FACTOR RECEPTOR 1 PRECURSOR (EC 2.7.1.112)			
DE	(FGFR-1) (BFGF-R) (MFR).			
GN	FGFR1 OR FLG.			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus			
OX	NCB1_TaxID=10116;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=93176824; PubMed=8382532;			
RA	Yasaki N., Hiroko F., Mitsuhiro O., Toshisuke K., Nobuyuki I.;			
RT	"The structure and expression of the GF receptor-1 mRNA isoforms in			
RT	rat tissues.";			
RL	Biochim. Biophys. Acta 1172:37-42(1993).			
CC	-!- FUNCTION: RECEPTOR FOR BASIC FIBROBLAST GROWTH FACTOR. A SHORTER			
CC	FORM OF THE RECEPTOR COULD BE A RECEPTOR FOR ACIDIC FGF (AFGF).			
CC	-!- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + PROTEIN			
CC	TYROSINE PHOSPHATE.			
CC	-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.			
CC	-!- SIMILARITY: BELONGS TO THE FIBROBLAST GROWTH FACTOR RECEPTOR			
CC	FAMILY.			

CC	-I SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC	-----
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CC	-----
DR	EMBL; D12498; BAA02059.1; -.
DR	PIR; S29840; S29840.
DR	HSSP; P11362; IEGI.
DR	InterPro; IPR000719; Euk_Pkinase.
DR	InterPro; IPR003006; Ig_MHC.
DR	InterPro; IPR003598; Ig_C2.
DR	InterPro; IPR001245; Tyr_Kin.
DR	Pfam; PF00047; Ig_3.
DR	Pfam; PF00069; Pkinase; 1.
DR	PRINTS; PR00109; TYRKINASE.
DR	SMART; SM00408; IGC2; 3.
DR	SMART; SM00219; TYRC; 1.
DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR	PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR	PROSITE; PSS0011; PROTEIN_KINASE_DOM; 1.
KW	Receptor; Glycoprotein; Tyrosine-protein kinase; ATP-binding;
KW	Transferrase; Phosphorylation; Transmembrane; Signal;
KW	Immunoglobulin domain.
FT	SIGNAL 1 21 POTENTIAL.
FT	CHAIN 22 822 BASIC FIBROBLAST GROWTH FACTOR RECEPTOR
FT	1.
FT	DOMAIN 22 376 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 377 397 POTENTIAL.
FT	DOMAIN 398 822 CYTOPLASMIC (POTENTIAL).
FT	DOMAIN 48 108 IG-LIKE C2-TYPE DOMAIN 1.
FT	DOMAIN 171 237 IG-LIKE C2-TYPE DOMAIN 2.
FT	DOMAIN 270 348 IG-LIKE C2-TYPE DOMAIN 3.
FT	DOMAIN 478 767 PROTEIN KINASE.
FT	NF-BIND 484 492 ATP (BY SIMILARITY).
FT	NF-BIND 484 492 ATP (BY SIMILARITY).
FT	BINDING 514 514 BY SIMILARITY.
FT	ACT_SITE 623 623 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT	MOD_RES 654 654 POTENTIAL.
FT	DISULEID 55 101 POTENTIAL.
FT	DISULEID 178 230 POTENTIAL.
FT	DISULEID 277 341 POTENTIAL.
FT	CARBOHYD 77 77 N-LINKED (GLCNAC... ) (POTENTIAL).
FT	CARBOHYD 117 117 N-LINKED (GLCNAC... ) (POTENTIAL).
FT	CARBOHYD 227 227 N-LINKED (GLCNAC... ) (POTENTIAL).
FT	CARBOHYD 240 240 N-LINKED (GLCNAC... ) (POTENTIAL).
FT	CARBOHYD 264 264 N-LINKED (GLCNAC... ) (POTENTIAL).
FT	CARBOHYD 296 296 N-LINKED (GLCNAC... ) (POTENTIAL).
FT	CARBOHYD 317 317 N-LINKED (GLCNAC... ) (POTENTIAL).
FT	CARBOHYD 330 330 N-LINKED (GLCNAC... ) (POTENTIAL).
SQ	SEQUENCE 822 AA; 91824 MW; E59924D0AIDESC5 CRC64;

		20.4%:	Score 362.5:	DB 1:	Length 822:
Query Match					
Best-Local Similarity		30.4%:	Pred. No. 4.1e-20:		
Matches: 89;	Conservative 44;	Mismatches 111;	Indels 49;	Gaps 9;	
QY	20	RPPF--PEARQKRTWSHSGRWAPGHCAAVPE-----GDPEPLTM-----	60		
DB	22	RPAPLPLEQAGPW-----GVPEVESLLVHPRDILQLGRCRLRDVQSI	64		
QY	61	-WTQSGRTIHSMSKFRRLPQGLKQYQVERDAGYVCSKATNGFSGLSVNTLYLVLDIS	119		
DB	65	NMLRDSVQIAES--NTRITRTGEEVVEROSIPADSGSLYAC--VTNSPSGSDTYTFEVSANSDLL	122		
QY	120	PGKESLGPDSSSGGQEDPA-----SQQWAPRPFPQPKMRRLVARYVGSVYRLCVIAG	174		
DB	123	PSEEDDDDDSSSEKETQDWTMKPRRRRVARYWISPEKMEKTKLHAYPAAKTYVAFKCPSSG	182		
QY	175	HRPDDITWKKDQALTRPE---AAEPKKKWTLSLKNLRPDSGKYTCVNSRAQAINA	230		

Db 183 TPSPFLRLKNGKEF-KPDHRIGGYKVRATWSTIMDSVPSDKGNVTCIYENENKGSINH 241

Qy 231 TYKDVIOFTRSKPYLGTHTPVNTVDFGGTTSPOCKRSDVKRYIOWMLKRYE 283

Db 242 TYOLDVRSRPHRPLDAGLPANKTVAGLSNVFVCKVYSDPOPHIOWMLKHE 294

RESULT 10

FGRL\_MOUSE STANDARD; PRT; 819 AA.

AC P21804;

DT 01-MAY-1991 (Rel. 18, Created)

DT 01-MAY-1991 (Rel. 18, Last sequence update)

DT 20-AUG-2001 (Rel. 40, Last annotation update)

DE BASIC FIBROBLAST GROWTH FACTOR RECEPTOR 1 PRECURSOR (EC 2.7.1.112).

GN CEN1.

OS Gallus gallus (Chicken).

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

NCBI\_TaxID=9031;

OX NCBI [1]

RP SEQUENCE FROM N.A.

RP MEDLINE=89315814; PubMed=2473471;

RA Pasquale E.B., Singer S.J.;

RT "Identification of a developmentally regulated protein-tyrosine kinase by using anti-phosphotyrosine antibodies to screen a cDNA expression library."

RT Proc. Natl. Acad. Sci. U.S.A. 86:5449-5453(1989).

RL [2]

RP REVISIONS.

RA Pasquale E.B.;

RL Submitted (MAY-1989) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RP MEDLINE=89298406; PubMed=254496;

RA Lee P.L., Johnson D.E., Consens L.S., Fried V.A., Williams L.T.;

RT "Purification and complementary DNA cloning of a receptor for basic fibroblast growth factor."

RL Science 245:57-60(1989).

CC -1- FUNCTION: RECEPTOR FOR BASIC FIBROBLAST GROWTH FACTOR.

CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE -> ADP + PROTEIN TYROSINE PHOSPHATE.

CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

CC -1- SIMILARITY: BELONGS TO THE FIBROBLAST GROWTH FACTOR RECEPTOR FAMILY.

CC -1- SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.

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CC EMBL; M24637; AAA48663.1; -

DR PIR; A41345; TVCHFG.

DR HSSP; P11362; IFGI.

DR InterPro; IPR000719; Euk\_Pkinase.

DR InterPro; IPR003006; Ig\_MHC.

DR InterPro; IPR003598; Ig\_C2.

DR InterPro; IPR001245; Tyr\_Kin.

DR Pfam; PF00047; Ig; 3.

DR Pfam; PF00069; Pkinase; 1.

DR PRINTS; PR00109; TYRKINASE.

DR SMART; SM00219; Tyrc; 3.

DR SMART; SM00408; IGC2; 3.

DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.

DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.

DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.

KW Receptor; Glycoprotein; Tyrosine-protein kinase; ATP-binding;

KW Transferase; Phosphorylation; Transmembrane; Immunoglobulin domain; Signal.

FT 1 21

FT SIGNAL

FT 22 819

FT CHAIN

FT 22 374

FT DOMAIN

FT 375 395

FT TRANSMEM

FT 396 819

FT DOMAIN

FT 47 108

FT DOMAIN

FT 169 235

FT DOMAIN

FT 268 346

FT DOMAIN

FT 125 132

FT DOMAIN

FT 476 765

FT NP\_BIND

FT 482 490

FT BINDING

FT 512 512

FT ACT\_SITE

FT 621 621

FT MOD\_RES

FT 652 652

FT DISULFID

FT 176 228

FT DISULFID

FT 275 339

FT CARBOHYD

FT 76 76

FT CARBOHYD

FT 116 116

FT CARBOHYD

FT 225 225

FT CARBOHYD

FT 238 238

FT CARBOHYD

FT 262 262

FT CARBOHYD

FT 294 294

FT CARBOHYD

FT 315 315

FT CARBOHYD

FT 328 328

FT CONFLICT

FT 90 90

SO SEQUENCE

819 AA; 91576 MW; 76030B7A5E181DDC CRC64;

Query Match 20.3%; Score 361.5; DB 1; Length 819;

Best Local Similarity 32.9%; Pred. No. 4.9e-20;

Matches 76; Conservative 44; Mismatches 100; Indels 11; Gaps 5;

Qy 61 WTKDSRTIHSGRFVPLGTHPVNTVDFGGTTSPOCKRSDVKRYIOWMLKRYE 120

Db 65 WVRDGVQLPEN-NKRTIRIGEEYERDAVPEDSGLACMTNSGSGS-ETTYSVNSDALP 122

Qy 121 GKESLGPDPSSGGQEDPSPS---QOMARPRFTOPSKMRRYIARVPGSSVRLKCYASGHP 176

Db 123 SAEDDDDDDDSSSEKEDNKRPNQAVAPYWTYPPEMKKHLAVPAATVTKCKSGSGHP 182

Qy 177 RPDITWKKDQALNRP-----AAEPKRRKWTLSLKNLRPDSGKTYCRVSRAGAINATY 232

Db 183 NPTLEMLKNGKEF-KPDHRIGGYKVRATWSTIMDSVPSDKGNVTCIYENENKGSINH 241

Qy 233 KYDVIOFTRSKPYLGTHTPVNTVDFGGTTSPOCKRSDVKRYIOWMLKRYE 283

Db 242 QLDVRSRPHRPLDAGLPANKTVAGLSNVFVCKVYSDPOPHIOWMLKHE 292

RESULT 11

FGRL\_MOUSE STANDARD; PRT; 821 AA.

AC P21803; O61342;

DT 01-MAY-1991 (Rel. 18, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 20-AUG-2001 (Rel. 40, Last annotation update)

DE FIBROBLAST GROWTH FACTOR RECEPTOR 2 PRECURSOR (EC 2.7.1.112) (FGFR-2)

GN (KERATINOCYTE GROWTH FACTOR RECEPTOR).

GN FGFR2 OR ECT1 OR BEK.

OS Mus musculus (Mouse).

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI\_TaxID=10090;

OX NCBI [1]

RP SEQUENCE FROM N.A. (LONG FORM).

RP TISSUE=Brain, and Liver;

RC MEDLINE=92228773; PubMed=1373495;

RX Mansukhani A., Dell'Era P., Moscattelli D., Kornbluth S., Hanafusa H., Basillico C.;

RT "Characterization of the murine BEK fibroblast growth factor (FGF)  
 RT receptor: activation by three members of the FGF family and  
 RT requirement for heparin.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 89:3305-3309(1992).  
 RN [2]  
 RP SEQUENCE FROM N.A. (SHORT FORM).  
 RX MEDLINE-91095977; PubMed-1846048;  
 RA Miki T., Fleming T.P., Bottaro D.P., Rubin J.S., Ron D.,  
 RA Aaronson S.A.;  
 RT "Expression cDNA cloning of the KGF receptor by creation of a  
 RT transforming autocrine loop.";  
 RL Science 251:72-75(1991).  
 RN [3]  
 RP SEQUENCE OF 477-821 FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE-89219016; PubMed-2468999;  
 RA Kornbluth S., Paulson K.E., Hanafusa H.;  
 RT "Novel tyrosine kinase identified by phosphotyrosine antibody  
 RT screening of cDNA libraries.";  
 RL Mol. Cell. Biol. 8:5541-5544(1988).  
 CC -1- FUNCTION: RECEPTOR FOR ACIDIC AND BASIC FIBROBLAST GROWTH FACTORS.  
 CC POSSESSES A HIGHER AFFINITY FOR ACIDIC THAN FOR BASIC FGF'S.  
 CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + PROTEIN  
 CC TYROSINE PHOSPHATE.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A  
 CC SHORT FORM, ARE PRODUCED BY ALTERNATIVE SPLICING.  
 CC -1- SIMILARITY: BELONGS TO THE FIBROBLAST GROWTH FACTOR RECEPTOR  
 CC FAMILY.  
 CC -1- SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 DR EMBL, M66441; AAA37286.1; -  
 DR EMBL, M63503; AAA39377.1; -  
 DR EMBL, M23362; AAA37285.1; -  
 DR PIR, A31378; TVMSBK.  
 DR PIR, A38428; A38429.  
 DR HSSP, P11362; 1FGI.  
 DR MGD, MG1:95523; Egit2.  
 DR InterPro: IPR000719; Euk\_pkinase.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003598; Ig\_C2.  
 DR InterPro: IPR001245; Tyr\_Kin.  
 DR Pfam, PF00047; 1g; 3.  
 DR Pfam, PF00069; pkinase; 1.  
 DR PRINTS: PR00109; TYRKINASE.  
 DR SMART: SM00408; IGC2; 3.  
 DR SMART: SM00219; TYRK; 1.  
 DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE: PS00109; PROTEIN\_KINASE\_TYR; 1.  
 DR PROSITE: PS00111; PROTEIN\_KINASE\_DOM; 1.  
 DR Receptor; Glycoprotein; Tyrosine-protein kinase; ATP-binding;  
 KW Transferrase; Phosphorylation; Transmembrane; Signal;  
 KM Immunoglobulin domain; Alternative splicing.  
 FT SIGNAL 1 21  
 FT CHAIN 1 21  
 FT FT 22 821 FIBROBLAST GROWTH FACTOR RECEPTOR 2.  
 FT DOMAIN 22 377 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 378 398 POTENTIAL.  
 FT DOMAIN 399 821 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 55 114 IG-LIKE C2-TYPE DOMAIN 1.  
 FT DOMAIN 172 238 IG-LIKE C2-TYPE DOMAIN 2.  
 FT DOMAIN 271 349 IG-LIKE C2-TYPE DOMAIN 3.  
 FT DOMAIN 481 770 PROTEIN KINASE.  
 FT NP\_BIND 487 495 ATP (BY SIMILARITY).  
 FT BINDING 517 517 ATP (BY SIMILARITY).  
 FT ACT\_SITE 626 626 BY SIMILARITY.

FT MOD\_RES 657 657 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).  
 FT DISULFID 62 107 POTENTIAL.  
 FT DISULFID 179 231 POTENTIAL.  
 FT DISULFID 278 342 POTENTIAL.  
 FT CARBOHYD 83 83 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 123 123 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 147 147 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 228 228 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 265 265 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 297 297 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 318 318 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 331 331 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT VARSPPLIC 37 37 E -> G (IN SHORT ISOFORM).  
 FT VARSPPLIC 38 152 MISSING (IN SHORT ISOFORM).  
 FT VARSPPLIC 314 361  
 FT CONFLICT 169 169  
 FT CONFLICT 187 187  
 FT SEQUENCE 821 AA; 91983 MW; FCD828ADD61FA414 CRC64;  
 SO  
 Query Match 20.3%; Score 361; DB 1; Length 821;  
 Best Local Similarity 32.0%; Pred. No. 5,3e-20;  
 Matches 87; Conservative 46; Mismatches 117; Indels 22; Gaps 6;  
 QY 23 PEAPAPQRWRWRHGWMPAGPHCAAAVPPDG-----DEPPLMTKTCGRTHSGMSRF 75  
 DB 35 PEEPPTRKYQI-----SPEEAYVVAPEGSELEQCLMDAAVISMTKD--VHLDPNNR 84  
 QY 76 RVL-POGLKRYQVERDAGYVCATNGFSLSVNTLVLDISPGKESIGPSSSGGQ 134  
 DB 85 TVLIGELYLQKGAITPRDSGLYACTARTYDSEIWMVNTDAISSGDEDDTDSSEDV 144  
 QY 135 EDPAQQMARPRTPQSKRRRYIAPVGVSVLKCVAASGHPPTITWAKDQALT---R 191  
 DB 145 SENRSQRA-PVYTNTEKMEKRLHACPAANTVYFRCPPAGNPSTWRMLKNGEFPQHR 203  
 QY 192 PEAAEPRKKKWTSLKLNRPEDSGKTCRVSNAAGINATYKVDVIOPTFRSKVLTGTHP 251  
 DB 204 IGGYKVRNQWLSLIMESVPSDKGNTCTCLVENYGSINHTYHLDVVERSHRPTLDAGLP 263  
 QY 252 VNTTVDEGGTSPQCKVRSDVYKPVLIQMKRVE 283  
 DB 264 ANASTVVGSDVEPVCVKVSDAQPHIQIKHVE 295  
 Db  
 RESULT 12  
 FGRL\_HUMAN STANDARD; PRT; 822 AA.  
 AC P11362; P17049;  
 DT 01-JUL-1989 (Rel. 11, Created)  
 DT 01-MAY-1991 (Rel. 18, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)  
 DE BASIC FIBROBLAST GROWTH FACTOR RECEPTOR 1 PRECURSOR (BC 2.7.1.112)  
 DE (FGFR-1) (BFGF-R) (FMS-LIKE TYROSINE KINASE-2) (C-FGR).  
 GN FGFR1 OR FLG OR FGFR OR FLT2.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=placenta;  
 RX MEDLINE-90245600; PubMed-2159626;  
 RA Isaacchi A., Bergonzoni L., Sarmientos P.;  
 RT "Complete sequence of a human receptor for acidic and basic  
 RT fibroblast growth factors.";  
 RL Nucleic Acids Res. 18:1906-1906(1990).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Neonatal brain stem;

RA MEDLINE=90360977; PubMed=1697263;  
RA Dione C.A., Crumley G.R., Bellot F., Kaplow J.M., Seafoss G.,  
RA Ruta M., Bugges W.H., Jaffe M., Schlessinger J.,  
RT "Cloning and expression of two distinct high-affinity receptors  
RT cross-reacting with acidic and basic fibroblast growth factors.";  
RL EMBL J. 9:2685-2692(1990).  
[3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92282615; PubMed=1317750;  
RA Hattori Y., Odagiri H., Katoh O., Sakamoto H., Morita T.,  
RA Shimotohno K., Tobinai K., Sugimura T., Terada M.,  
RT "s-sam-related gene, N-sam, encodes fibroblast growth factor receptor  
RT and is expressed in T-lymphocytic tumors.";  
RL Cancer Res. 52:3367-3371(1992).  
[4]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
RX MEDLINE=91126480; PubMed=1846977;  
RA Hou J., Kan M., McKeenan K., McBride G., Adams P., McKeenan W.L.,  
RT "Fibroblast growth factor receptors from liver vary in three  
RT structural domains.";  
RL Science 251:665-668(1991).  
[5]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92118399; PubMed=1662973;  
RA Klefer M.C., Baird A., George-Nascimento C., Nguyen T., Mason O.B.,  
RA Boley L.J., Valenzuela P., Barr P.J.,  
RT "Molecular cloning of a human basic fibroblast growth factor receptor  
RT cDNA and expression of a biologically active extracellular domain in  
RT a baculovirus system.";  
RL Growth Factors 5:115-127(1991).  
[6]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Placenta;  
RX MEDLINE=90290512; PubMed=2162671;  
RA Itoh N., Terachi T., Ohta M., Seo M.K.,  
RT "The complete amino acid sequence of the shorter form of human basic  
RT fibroblast growth factor receptor deduced from its cDNA.";  
RL Biochem. Biophys. Res. Commun. 169:680-685(1990).  
[7]  
RP SEQUENCE OF 201-822 FROM N.A.  
RA Rita M., Hawk R., Rizza G., Drohan W., Zabelshansky M., Laureys G.,  
RA Barton D.E., Francke U., Schlessinger J., Glvol D.,  
RT "A novel protein tyrosine kinase gene whose expression is modulated  
RT during endothelial cell differentiation.";  
RL Oncogene 3:9-15(1988).  
[8]  
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.  
RX MEDLINE=90355989; PubMed=2167437;  
RA Johnson D.E., Lee P.L., Lu J., Williams L.T.,  
RT "Inverse forms of a receptor for acidic and basic fibroblast growth  
RT factors.";  
RL Mol. Cell. Biol. 10:4728-4736(1990).  
[9]  
RP ALTERNATIVE SPLICING.  
RX MEDLINE=91141499; PubMed=1847500;  
RA Gutkind S.J., Link D.C., Katamine S., Lacal P., Miki T., Ley T.J.,  
RA Robbins K.C.,  
RT "A novel c-fgr exon utilized in Epstein-Barr virus-infected B  
RT lymphocytes but not in normal monocytes.";  
RL Mol. Cell. Biol. 11:1500-1507(1991).  
[10]  
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.  
RC TISSUE=Lung;  
RX MEDLINE=91319400; PubMed=1650441;  
RA Eisenmann A., Ahn J.A., Graziani G., Tronick S.R., Ron D.,  
RT "Alternative splicing generates at least five different isoforms of  
RT the human basic-FGF receptor.";  
RL Oncogene 6:1195-1202(1991).  
[11]  
RP SEQUENCE FROM N.A.  
RA Wenstrom S., Sandstrom C., Claesson-Welsh L.,  
RT Submitted (JUL-1990) to the EMBL/GenBank/DBJ databases.

RN [12]  
RP MUTAGENESIS OF TYR-766.  
RX MEDLINE=92357144; PubMed=1379697;  
RA Peters K.G., Marie J., Wilson E., Ives H.E., Escobedo J.,  
RA del Rosario M., Mirda D., Williams L.T.,  
RT "Point mutation of an FGF receptor abolishes phosphatidylinositol  
RT turnover and Ca2+ flux but not mitogenesis.";  
RL Nature 358:678-681(1992).  
[13]  
RP MUTAGENESIS OF TYR-766.  
RX MEDLINE=92357145; PubMed=1379698;  
RA Mohammadi M., Dione C.A., Li W., Lin N., Spivak T., Honegger A.M.,  
RA Jaffe M., Schlessinger J.,  
RT "Point mutation in FGF receptor eliminates phosphatidylinositol  
RT hydrolysis without affecting mitogenesis.";  
RL Nature 358:681-684(1992).  
[14]  
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 464-762.  
RX MEDLINE=96361355; PubMed=8752212;  
RA Mohammadi M., Schlessinger J., Hubbard S.R.,  
RT "Structure of the FGF receptor tyrosine kinase domain reveals a novel  
RT autoinhibitory mechanism.";  
RL Cell 86:577-587(1996).  
[15]  
RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 464-762.  
RX MEDLINE=97284786; PubMed=9139660;  
RA Mohammadi M., McMahon G., Sun L., Tang C., Hirth P., Yeh B.K.,  
RA Hubbard S.R., Schlessinger J.,  
RT "Structures of the tyrosine kinase domain of fibroblast growth factor  
RT receptor in complex with inhibitors.";  
RL Science 276:955-960(1997).  
[16]  
RP VARIANT PREEIFER SYNDROME ARG-252.  
RX MEDLINE=95179173; PubMed=7874169;  
RA Muenke M., Scheil U., Hehr A., Robin N.H., Losken H.W., Schinzel A.,  
RA Pullen L.J., Rutland P., Reardon W., Malcolm S., Winter R.M.,  
RT "A common mutation in the fibroblast growth factor receptor 1 gene in  
RT Pfeiffer syndrome.";  
RL Nat. Genet. 8:269-274(1994).  
CC -1- FUNCTION: RECEPTOR FOR BASIC FIBROBLAST GROWTH FACTOR. A SHORTER  
CC FORM OF THE RECEPTOR COULD BE A RECEPTOR FOR ACIDIC FGF (ARFGF).  
CC -1- CATALYTIC ACTIVITY: ATP + PROTEIN TYROSINE = ADP + PROTEIN  
CC TYROSINE PHOSPHATE.  
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
CC -1- ALTERNATIVE PRODUCTS: MANY FORMS OF FGFR1 ARE PRODUCED BY  
CC ALTERNATIVE SPLICING. THE FORM SHOWN HERE IS KNOWN AS ALPHA-A1.  
CC -1- DISEASE: DEFECTS IN FGFR1 ARE ONE OF THE CAUSES OF PEEIFER  
CC SYNDROME (FS) (ALSO KNOWN AS ACROCEPHALOSYNDACTYL TYPE V; ACS5);  
CC CHARACTERIZED BY CRANIOSYNOSTOSIS (PREMATURE FUSION OF THE SKULL  
CC SUTURES) WITH DEVIATION AND ENLARGEMENT OF THE THUMBS AND GREAT  
CC TOES, BRACHYMESEPHALANGY, WITH PALANGEAL ANKLYOSIS AND A VARYING  
CC DEGREE OF SOFT TISSUE SYNDACTYL.  
CC -1- SIMILARITY: BELONGS TO THE FIBROBLAST GROWTH FACTOR RECEPTOR  
CC FAMILY.  
CC -1- SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL: X51803; CA36101.1; -  
DR EMBL: X52833; CA37015.1; -  
DR EMBL: X66945; CA47375.1; -  
DR EMBL: Y00665; CA68679.1; -  
DR EMBL: M37722; AAA75007.1; -  
DR EMBL: M60485; AAA35840.1; -  
DR EMBL: M63887; AAA35958.1; -  
DR EMBL: M34185; AAA35836.1; -  
DR EMBL: M34186; AAA35837.1; -

DR EMBL: X57118; CAA40400.1; ALT\_TERM.  
 DR EMBL: X57119; CAA40401.1; -  
 DR EMBL: X57120; CAA40402.1; -  
 DR EMBL: X57121; CAA40403.1; -  
 DR EMBL: X57122; CAA40404.1; -  
 DR EMBL: M34641; AAA35835.1; -  
 DR EMBL: A29216; CAA01958.1; -  
 DR PIR: S11692; TVHUFQ.  
 DR PIR: S25420; S25420.  
 DR PIR: S26739; S26739.  
 DR PDB: 1FGK; 23-JUL-97.  
 DR PDB: 1FGL; 08-APR-98.  
 DR PDB: 1AGW; 25-MAR-98.  
 DR MIM: 136350; -  
 DR MIM: 101600; -  
 DR InterPro: IPR000719; Euk\_Pkinase.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003598; Ig\_c2.  
 DR InterPro: IPR001245; Tyr\_kin.  
 DR Pfam: PF00047; 19; 3.  
 DR Pfam: PF00069; pkinase.1.  
 DR PRINTS: PR00109; TYRKINASE.  
 DR SMART: SM00408; Igc2; 3.  
 DR SMART: SM00219; TyKc; 1.  
 DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE: PS00109; PROTEIN\_KINASE\_TYR; 1.  
 DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR Receptor: Glycoprotein: Tyrosine-protein kinase; ATP-binding;  
 KW transferase; Phosphorylation; Transmembrane; Signal; 3D-structure;  
 KM immunoglobulin domain; Alternative splicing; Disease mutation.  
 FT SIGNAL 1 21 POTENTIAL.

Query Match 20.3%; Score 360.5; DB 1; Length 822;  
 Best Local Similarity 29.9%; Pred. No. 5, 8e-20;  
 Matches 87; Conservative 45; Mismatches 114; Indels 45; Gaps 8;

QY 20 RPP--PEAQRMTKSHGRWPAHPHCAAVPEG-----DPPPLTW 61  
 DB 22 RPSPTLEEQAPW-----GAPVESEFLVHPGDLQLQRCLRDVQISIN 66  
 QY 62 TRGGRTHSGWSRPRVLPGLAKYQVEREDAGYVCATNGFSLSNVYLLVLDISPG 121  
 DB 67 LRGVQALAE-NRTIRIGEVEVDSPADSGIACVTSPPSS-DTTFYSVNSDLPS 124  
 QY 122 KESLGPDSGGQEDPA-----SQOMARPRFTOPSKMRRIARPVSSYRLKCVASGHP 176  
 DB 125 SEDDDDDSSSEKETDNTKPRMPVAPYVTSPEKKEKLLHVPRAKTYKFCPSGTP 184  
 QY 177 RPIITVMKDDQALTRP-----AAEPKKKWTLLKLRPDSGKTYCRVSNRAINATY 232  
 DB 185 NPTLRMLKNGKEF-KPDHRIIGYKVRATWSILMDSVPSDKNGNYTCIVENEYSINHTY 243  
 QY 233 KVDVIORTSRKPYLTGTHPYNTVDFGCTSFQCKVRSQDKPYIOWMKRRE 283  
 DB 244 QLDVERSPHRIPLQAGLPAKNTVALGSSNVEKCKVYSDPHIOWLKITE 294

RESULT 13  
 FGR4\_MOUSE STANDARD: PRT: 808 AA.  
 AC 003142:  
 DT 01-OCT-1994 (rel. 30, Created)  
 DT 01-OCT-1996 (rel. 34, Last sequence update)  
 DT 20-AUG-2001 (rel. 40, Last annotation update)  
 DE FIBROBLAST GROWTH FACTOR RECEPTOR 4 PRECURSOR (EC 2.7.1.112) (FGR-4)  
 DE (PROTEIN-TYROSINE KINASE RECEPTOR MPK-11).  
 GN FGR4 OR FGR-4 OR MPK-11.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxId=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RC STRAIN-CD-1: TISSUE-Fetal cerebellum;  
 RX MEDLINE-92146274; PubMed-1723680;  
 RA Stark K.L., McMahon J., McMahon A.P.;  
 RT "FGR-4, a new member of the fibroblast growth factor receptor  
 RT family, expressed in the definitive endoderm and skeletal muscle  
 RT lineages of the mouse."  
 RL Development 113:641-651(1992).  
 RN [2]  
 RP SEQUENCE OF 620-676 FROM N.A.  
 RC STRAIN-C57BL; TISSUE-Embryonic brain;  
 RX MEDLINE-93096484; PubMed-1281307;  
 RA Giliardi-Hebenstreit P., Nieto M.A., Fraim M., Mattei M.-G.,  
 RA Chastier A., Wilkinson D.G., Charnay P.;  
 RT "An Eph-related receptor protein tyrosine kinase gene segmentally  
 RT expressed in the developing mouse hindbrain."  
 RL Oncogene 7:2499-2506(1992).  
 CC -1- FUNCTION: PUTATIVE RECEPTOR FOR BASIC FIBROBLAST GROWTH FACTOR.  
 CC MAY BE INVOLVED IN THE DEVELOPMENT OF SKELETAL MUSCLE CELL  
 CC LINEAGES.  
 CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + PROTEIN  
 CC TYROSINE PHOSPHATE.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN THE DEVELOPING GUT ENDODERM,  
 CC IN MYOTOMALLY DERIVED SKELETAL MUSCLE, THE ADRENAL CORTEX,  
 CC KIDNEY AND CONDENSING CARTILAGE. PRESENT IN ADULT LIVER,  
 CC LUNG AND KIDNEY.  
 CC -1- SIMILARITY: BELONGS TO THE FIBROBLAST GROWTH FACTOR RECEPTOR  
 CC FAMILY.  
 CC -1- SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.  
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 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC EMBL: X59927; CAA42551.1; -  
 DR EMBL: X57236; CAA40512.1; -  
 DR HSSP: P11362; 1FGI.  
 DR MGD: MGI:95525; Fgfr4.  
 DR InterPro: IPR000719; Euk\_Pkinase.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003598; Ig\_c2.  
 DR InterPro: IPR001245; Tyr\_kin.  
 DR Pfam: PF00047; 19; 3.  
 DR Pfam: PF00069; pkinase.2.  
 DR PRINTS: PR00109; TYRKINASE.  
 DR SMART: SM00408; Igc2; 3.  
 DR SMART: SM00219; TyKc; 1.  
 DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; FALSE\_NEG.  
 DR PROSITE: PS00109; PROTEIN\_KINASE\_TYR; 1.  
 DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
 KW Receptor; Glycoprotein; Tyrosine-protein kinase; ATP-binding;  
 KW transferase; Phosphorylation; Transmembrane; Immunoglobulin domain;  
 KW Signal.  
 FT SIGNAL 1 18  
 FT CHAIN 19 808  
 FT DOMAIN 19 366  
 FT TRANSMEM 367 387  
 FT DOMAIN 388 808  
 FT DOMAIN 53 98  
 FT DOMAIN 169 221  
 FT DOMAIN 268 330  
 FT DOMAIN 464 761  
 FT NP\_BIND 470 478  
 FT BINDING 509 509  
 FT ACT\_SITE 618 618  
 FT MOD\_RES 649 649  
 FT DISULFID 53 98  
 FT DISULFID 169 221  
 FT DISULFID 268 330  
 FT POTENTIAL.  
 FT FIBROBLAST GROWTH FACTOR RECEPTOR 4.  
 FT EXTRACELLULAR (POTENTIAL).  
 FT POTENTIAL.  
 FT CYTOPLASMIC (POTENTIAL).  
 FT IG-LIKE C2-TYPE DOMAIN 1.  
 FT IG-LIKE C2-TYPE DOMAIN 2.  
 FT IG-LIKE C2-TYPE DOMAIN 3.  
 FT PROTEIN KINASE.  
 FT ATP (BY SIMILARITY).  
 FT BINDING.  
 FT BY SIMILARITY.  
 FT PHOSPHORYLATION (AUTO-) (BY SIMILARITY).  
 FT POTENTIAL.  
 FT POTENTIAL.  
 FT POTENTIAL.

FT CARBOHYD 109 109 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 255 255 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 287 287 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 308 308 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 319 319 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 808 AA; 89775 MW; E3F30BE5E334E8B6 CRC64;

Query Match 20.2%; Score 358.5; DB 1; Length 808;  
 Best Local Similarity 33.0%; Pred. No. 8.1e-20;  
 Matches 100; Conservative 44; Mismatches 108; Indels 51; Gaps 11;

QY 37 GRWAPHCACAAVVEEDPRLMTKDGRTIHS-----GMSRRPVLPQGLKVKOVERED 91  
 DB 55 GRTERGHN-----WYKEGSLASAGVRGM-RGR-----LEISFLPED 92  
 QY 92 AGVYCATNGEGSLVNYTLVLDD-----ISPGKESLGPDSGGQEDPASQOMAPR 146  
 DB 93 AGRYLCLAR--GSMYVHNLTLLMDSLTISNDEDEPKLTSSSSGHVYP--QQ--APY 145  
 QY 147 FTQSKMRRIARIPVSSSVRLKCVASGHRPDITMVKDOAL--TRPEAAERKKKWT 203  
 DB 146 WTHQORREKTLHAAPVACNTPVFCRCPACRNMPPTIHLKDGAFEGENIGIRLRHOMWS 205  
 QY 204 LSLKRLPEDSGKYTCRVSNRAGAIINATYKVDVIOFTRSKPVLGTFHPNTTVDGEGTTS 263  
 DB 206 LYMSSVPSDRTGYTCLVENSLSGIRSYLLDLVERSHRILLAGLPANTTAAGSVYE 265  
 QY 264 FQCKVRSDVKFVIOMLKRV-----EYGAEG-----RHNSITDVGOKFVPLPTGWSRPD 314  
 DB 266 LKCKVSDAQHIQMLKHVINGSSFGADGPYQVLTKTIDINISEVQVLTLRVNSADA 325  
 QY 315 GSY 317  
 DB 326 GEY 328

RESULT 14  
 FGR2\_XENLA STANDARD; PRT; 813 AA.  
 ID FGR2\_XENLA  
 AC 003364;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)  
 DE FIBROBLAST GROWTH FACTOR RECEPTOR 2 PRECURSOR (EC 2.7.1.112).  
 GN FGR2.  
 OS Xenopus laevis (African clawed frog).  
 OC Amphibia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Xenopodidae; Xenopus.  
 OX NCBI\_Taxid=8355;

RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93201992; PubMed=1284237;  
 RA Friesel R., Brown S.A.N.;  
 RT "Spatially restricted expression of fibroblast growth factor  
 receptor-2 during xenopus development.";  
 RL Development 116:1051-1058(1992).  
 CC -1- FUNCTION: RECEPTOR FOR ACIDIC AND BASIC FIBROBLAST GROWTH  
 CC FACTORS.  
 CC CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + PROTEIN  
 CC TYROSINE PHOSPHATE.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN THE ANTERIOR NEURAL PLATE  
 CC IN EARLY NEURULA STAGE EMBRYOS. LATER IN DEVELOPMENT, THE  
 CC PROTEIN IS ALSO EXPRESSED IN THE EYE ANLAGEN, MIDBRAIN-HINDBRAIN  
 CC BOUNDARY AND OTIC VESICLE.  
 CC -1- SIMILARITY: BELONGS TO THE FIBROBLAST GROWTH FACTOR RECEPTOR  
 CC FAMILY.  
 CC -1- SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.  
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DR EMBL: X65943; CAA64758.1; -  
 DR PIR: S25060; S25060.  
 DR HSP; P11362; ITC1.  
 DR InterPro: IPR000719; Euk\_Pkinase.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003598; Ig\_C2.  
 DR InterPro: IPR001245; Tyr\_kin.  
 DR Pfam: PF00064; Ig\_3.  
 DR Pfam: PF00069; Pkinase.1.  
 DR PRINTS; PR00109; TYRKINASE.  
 DR SMART; SM00408; IGC2; 3.  
 DR SMART; SM00219; TYRC; 1.  
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.  
 DR PROSITE; PS00109; PROTEIN KINASE TYR; 1.  
 DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.  
 DR Receptor; Glycoprotein; Tyrosine-protein kinase; ATP-binding;  
 KW Transferase; Phosphorylation; Transmembrane; Immunoglobulin domain;  
 KW Signal.  
 FT SIGNAL 1 14  
 FT CHAIN 15 813  
 FT DOMAIN 18 367  
 FT TRANSMEM 368 388  
 FT DOMAIN 389 813  
 FT DOMAIN 51 106  
 FT DOMAIN 163 228  
 FT DOMAIN 261 339  
 FT DOMAIN 471 760  
 FT NP\_BIND 477 485  
 FT BINDING 507 507  
 FT ACT\_SITE 616 616  
 FT MOD\_RES 647 647  
 FT CARBOHYD 79 79  
 FT CARBOHYD 115 115  
 FT CARBOHYD 231 231  
 FT CARBOHYD 255 255  
 FT CARBOHYD 287 287  
 FT CARBOHYD 308 308  
 FT CARBOHYD 321 321  
 SQ SEQUENCE 813 AA; 91340 MW; 81543656892A565 CRC64;

Query Match 18.8%; Score 334.5; DB 1; Length 813;  
 Best Local Similarity 29.5%; Pred. No. 5.3e-18;  
 Matches 87; Conservative 46; Mismatches 107; Indels 55; Gaps 10;

QY 21 PPPPEAPQRMRTKMSHGMPAGHCACAAVY-EGDP-----PPLMTTKDGRTHS 70  
 DB 29 PEPEPPAKYQI-----SKADVFPVLPGBDLRLCPDLAGPLVTWTKDGAKLEV 77  
 QY 71 GMSRRPVLPQGLKVKOVERDAGYVCKATNGFGLSNVTLVLVDDISPKESEGPSS 130  
 DB 78 N-NRLIVRTYLOIKESTTRDSGLYACSVLRNSHFHNVT-----EASS 121  
 QY 131 SGGEED--PASQOMAR-----PRETPSKMRRIARIPVSSSVRLKCVASGHRPDIT 181  
 DB 122 SGDEEDDDGSEDFDNNNNIRAPYWTTEKMEKTLHAASANYKLCPAR-BEPSPNE 180  
 QY 182 WMKDQALT--RPEAARPKKWTLSKLNRPEDSGKYTCRVSNRAGAIINATYKVDVIO 238  
 DB 181 WLKNGEKQKHRIIGGYKVRNOHWSLIMESVPSDKGYTCIVERHSHNHTYLDVIE 240  
 QY 239 FTRSKPVLTGHPVNTYVDEGTTSPCKVSDVKFVIOMLKRV-----YGAG 288  
 DB 241 RSSHRPILQAGLPANTTAAGVGDAEFYCKVYSDAQPHIRWVRIEKNKSGRGVDG 295

RESULT 15

BFR2\_HUMAN STANDARD; PRT; 654 AA.

ID BFR2\_HUMAN STANDARD; PRT; 654 AA.

AC 001742;

DT 01-JUL-1993 (Rel. 26, Created)

DT 20-AUG-2001 (Rel. 40, Last annotation update)

DE FIBROBLAST GROWTH FACTOR RECEPTOR BFR-2 PRECURSOR (EC 2.7.1.112).

GN BFR2.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

NCBI\_TaxId=9606;

LN [1]

RP MEDLINE=91274356; PubMed=1647213;

RA Seno M., Sasada R., Matanabe T., Ishimaru K., Igatahi K.;

RT Blochim. Biophys. Acta 1089:244-246(1991).

RL

CC -1- FUNCTION: RECEPTOR FOR ACIDIC AND BASIC FIBROBLAST GROWTH FACTORS.

CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + PROTEIN TYROSINE PHOSPHATE.

CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

CC -1- SIMILARITY: BELONGS TO THE FIBROBLAST GROWTH FACTOR RECEPTOR FAMILY.

CC -1- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.

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CC

EMBL: X56191; -- NOT\_ANNOTATED\_CDS.

DR HSSP: P11362; 1FGT.

DR InterPro: IPR000719; Euk\_PKinase.

DR InterPro: IPR003006; Ig\_MHC.

DR InterPro: IPR003598; Ig\_C2.

DR InterPro: IPR001245; Tyr\_Kin.

DR Pfam: PF00067; Ig\_2.

DR Pfam: PF00069; PKinase; 1.

DR PRINTS: PR00109; TYRKINASE.

DR SMART: SM00408; IGC2; 2.

DR SMART: SM00219; TYKC; 1.

DR PROSITE: PS00109; PROTEIN\_KINASE\_ATP; 1.

DR PROSITE: PS00109; PROTEIN\_KINASE\_TYR; 1.

DR PROSITE: PS00111; PROTEIN\_KINASE\_DOM; 1.

DR PROSITE: PS00111; Tyrosine-protein kinase; ATP-binding; Receptor; Glycoprotein; Tyrosine-protein kinase; Transmembrane; Immunoglobulin domain; Transferase; Phosphorylation; Transmembrane; Immunoglobulin domain;

DR

KW Signal.

FT SIGNAL 1 21

FT CHAIN 22 654

FT DOMAIN 22 263

FT TRANSMEM 264 284

FT DOMAIN 285 654

FT DOMAIN 57 123

FT DOMAIN 156 234

FT DOMAIN 367 647

FT NP\_BIND 373 381

FT BINDING 403 403

FT ACT\_SITE 512 512

FT MOD\_RES 543 543

FT CARBOHYD 113 113

FT CARBOHYD 126 126

FT CARBOHYD 130 130

FT CARBOHYD 182 182

FT CARBOHYD 203 203

FT CARBOHYD 214 214

FT CARBOHYD 235 235

SO SEQUENCE 654 AA; 73594 MW; F4954E7DC70FD233 CRC64;

Query Match 17.38; Score 307; DB 1; Length 654;

Best Local Similarity 29.38; Pred. No. 5e-16;

Matches 72; Conservative 43; Mismatches 89; Indels 42; Gaps 6;

QY 93 GVYCKATNFGSLV---NYTLVLLDISPKESLPDSSSGQEDPAQGMARPRFTQ 149

DB 5 GRFICLVVVMATLSLARPSLSLV-----ETTLEPECAPWTN 43

QY 150 PSKRRRVVIAKPVGSSVRLKCVASGHPDPITWKKDQALT--RPAAPRRKKWTLSL 206

DB 44 TEKMERLHAIVPANTVKEFCFAGGNMPTMRWLKNGKEFEQHRIGGYVRNOMSLIM 103

QY 207 KNLPEEDSGKYTCRVSNRAAIAATYKVDVYQRTSRKPVLTGHPVNTYDFGTTSFQC 266

DB 104 ESVVPSDKNGNTCVENEYSINHTYLDVRSPPRPILQAGLPANASTVVGQDFEVC 163

QY 267 KVSVDKPVVITLKRVE---YGAEG-----RHSTIDVGQKRVLPPTGQVMSRPD 314

DB 164 KYVSDAQPHQWIKHVKNSKYGPDGLPYLKYKHSQ---INSSNAEVLALFRVTEADA 220

QY 315 GSTYLNK 320

DB 221 GEYICK 226

RESULT 16

LAR.DROME STANDARD; PRT; 2029 AA.

ID LAR.DROME STANDARD; PRT; 2029 AA.

AC P16621;

DT 01-AUG-1990 (Rel. 15, Created)

DT 01-AUG-1990 (Rel. 15, Last sequence update)

DT 20-AUG-2001 (Rel. 40, Last annotation update)

DE PROTEIN-TYROSINE PHOSPHATASE DIAR PRECURSOR (EC 3.1.3.48) (PROTEIN-TYROSINE-PHOSPHATE PHOSPHOTROLASE).

GN LAR.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

NCBI\_TaxId=7227;

OX

RN [1]

RP SEQUENCE FROM N.A.

RA MEDLINE=90046860; PubMed=2554325;

RA Streuli M., Krueger N.X., Tsai A.Y.M., Saito H.;

RT "A family of receptor-linked protein tyrosine phosphatases in humans and Drosophila."

RL Proc. Natl. Acad. Sci. U.S.A. 86:8698-8702(1989).

RN [2]

RP SEQUENCE FROM N.A.

RA STRAIN-CANTON-S;

RX MEDLINE=96178473; PubMed=8598047;

RA Krueger N.X., van Vactor D., Wan H.I., Gelbart W.M., Goodman C.S., Saito H.;

RT "The transmembrane tyrosine phosphatase DIAR controls motor axon guidance in Drosophila."

RL Cell 84:611-622(1996).

CC -1- FUNCTION: IT IS POSSIBLE THAT DIAR IS A CELL ADHESION RECEPTOR. IT POSSESSES AN INTRINSIC PROTEIN TYROSINE PHOSPHATASE ACTIVITY (PTPASE). IT CONTROLS MOTOR AXON GUIDANCE.

CC -1- CATALYTIC ACTIVITY: PROTEIN TYROSINE PHOSPHATE + H(2)O = PROTEIN TYROSINE + ORTHOPHOSPHATE.

CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

CC -1- TISSUE SPECIFICITY: SELECTIVELY EXPRESSED IN A SUBSET OF AXONS AND PIONEER NEURONS IN THE EMBRYO.

CC -1- SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.

CC -1- SIMILARITY: CONTAINS 16 FIBRONECTIN TYPE III-LIKE DOMAINS.

CC -1- SIMILARITY: CONTAINS 2 PROTEIN-TYROSINE PHOSPHATASE DOMAINS.

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RT proteins provides no evidence for exon shuffling events after the  
RT separation of arthropod and chordate lineages.";  
RL Gene 215:47-55(1998).  
[3]  
RN REVISIONS.  
RA Hortsch M.;  
RL submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE FROM N.A. (SHORT ISOFORM).  
RC STRAIN-BERKELEY;  
RX MEDLINE=20196006; PubMed=10731132;  
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
Brandon R.C., Rogers Y.-H.C., Blaise R.G., Champe M., Pfeiffer B.D.,  
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
Abail J.F., Agbayani A., An H.-J., Andrews-Pfankoch C., Baldwin D.,  
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,  
Butlis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
Dudin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
Glodek A., Gong F., Gottrell J.H., Gu Z., Guan P., Harris M.,  
Harris N.L., Harvey D., Heilmann T.J., Hernandez J.R., Houck J.,  
Houston D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
Jaitai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
Kimmel B.E., Kodaira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
Lako P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
Lin X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacle J.M.,  
Palazzo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,  
Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
Ye J., Yen R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
Zheng X.H., Zhong F.-N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
RT "The genome sequence of Drosophila melanogaster.";  
RL Science 287:2185-2195(2000).  
[5]  
RN SEQUENCE OF 1182-1302 FROM N.A., AND CHARACTERIZATION.  
RP TISSUE-Embryo;  
RX MEDLINE=90262720; PubMed=1693086;  
RA Hortsch M., Bieher A.J., Patel N.H., Goodman C.S.;  
RT "Differential splicing generates a nervous system-specific form of  
Drosophila neuroglian.";  
RL Neuron 4:697-709(1990).  
RN [6]  
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 610-814.  
RX MEDLINE=94213741; PubMed=7512815;  
RA Huber A.H., Wang Y.-M.E., Bieher A.J., Bjorkman P.J.;  
RT "Crystal structure of tandem type III fibronectin domains from  
Drosophila neuroglian at 2.0 A.";  
RL Neuron 12:717-731(1994).  
CC -1- FUNCTION: THE LONG ISOFORM MAY PLAY A ROLE IN NEURAL AND GLIAL  
CELL ADHESION IN THE DEVELOPING EMBRYO. THE SHORT ISOFORM MAY BE A  
MORE GENERAL CELL ADHESION MOLECULE INVOLVED IN OTHER TISSUES AND  
IMAGINAL DISK MORPHOGENESIS. VITAL FOR EMBRYONIC DEVELOPMENT.  
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A  
SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.  
CC -1- TISSUE SPECIFICITY: LONG ISOFORM IS RESTRICTED TO SURFACE OF  
NEURONS AND GLIA IN THE DEVELOPING NERVOUS SYSTEM AND THE SHORT

CC ISOFORM TO OTHER NONNEURONAL TISSUES.  
CC -1- SIMILARITY: CONTAINS 6 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.  
CC -1- SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS.  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; M28231; AAA28728.2; -;  
DR EMBL; AF050085; AAC28613.2; -;  
DR EMBL; AF050084; AAC28613.2; JOINED.  
DR EMBL; AF050085; AAC28614.2; -;  
DR EMBL; AF050084; AAC28614.2; JOINED.  
DR EMBL; AF050344; AAC28617.1; -;  
DR EMBL; X76243; CAA53822.1; -;  
DR EMBL; X76244; CAA53823.1; -;  
DR PIR; A32579; A32579.  
DR PDB; 1CFB; 30-NOV-94.  
DR Flybase; FBgn0002968; Nrg.  
DR InterPro; IPR001777; FN\_III.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003598; IG\_C2.  
DR InterPro; IPR003600; IG\_Like.  
DR Pfam; PF00041; In3; 5.  
DR Pfam; PF00047; Ig; 6.  
DR PRINTS; PR00014; FNTYPEIII.  
DR SMART; SM00060; FN3; 5.  
DR SMART; SM00408; IGc2; 4.  
DR SMART; SM00410; IG\_Like; 2.  
KW Cell adhesion; Glycoprotein; Transmembrane; Repeat; 3D-structure;  
KW Immunoglobulin domain; Signal; Developmental protein;  
KW Alternative splicing.  
FT SIGNAL 1 23  
FT CHAIN 24 1302  
FT DOMAIN 24 1138  
FT TRANSMEM 1139 1154  
FT DOMAIN 1155 1302  
FT DOMAIN 53 123  
FT DOMAIN 149 224  
FT DOMAIN 262 329  
FT DOMAIN 354 422  
FT DOMAIN 447 512  
FT DOMAIN 536 606  
FT DOMAIN 629 690  
FT DOMAIN 729 792  
FT DOMAIN 832 896  
FT DOMAIN 932 997  
FT DOMAIN 1024 1098  
FT DISULFID 59 111  
FT CARBOHYD 625 706  
FT CARBOHYD 182 182  
FT CARBOHYD 188 198  
FT CARBOHYD 411 411  
FT CARBOHYD 448 448  
FT CARBOHYD 652 652  
FT CARBOHYD 683 683  
FT CARBOHYD 821 821  
FT CARBOHYD 1125 1125  
FT VARSPLIC 1224 1239  
FT VARSPLIC 1240 1302  
FT VARSPLIC 85 86  
FT CONFLICT 1282 1282  
FT SEQUENCE 1302 AA; 143617 MW; 59BD9DF286F5681A CRC64;  
Query Match 12.6%; Score 225; DB 1; Length 1302;  
Best Local Similarity 24.9%; Pred. No. 1.8e-09;  
Matches 70; Conservative 43; Mismatches 98; Indels 70; Gaps 12;



FT	DISULFID	2456	2506	BY SIMILARITY.
FT	DISULFID	2554	2599	BY SIMILARITY.
FT	DISULFID	2641	2686	BY SIMILARITY.
FT	DISULFID	2831	2876	BY SIMILARITY.
FT	DISULFID	2917	2962	BY SIMILARITY.
Query Match				
Best Local Similarity		12.6%	Score 224;	DB 1; Length 3707;
Matches		82; Conservative	34; Mismatches	77; Indels 90; Gaps
OY	44 HCAAAVPEGDDEPPLMTWTKDGRTHSGSRFRV-LP-----	OGLKQVEREDAGV	95	
DB	2553 HCSAI-----GNPP-----	TIH--WSKLRAPLPMQHRLEGNTLVIPRAQDSQGY	25	
OY	96 VCKATNGFSGLSVNTLVLLVDLIDISPKBSLGPDSSSGGQEDPASQOMARPRFQPSKMR	15		
DB	2598 ICAHTNLSAGHTEAT---VYLHVESPPYATIIPEHTS-----	26		
OY	156 RYIARPVSSVRKLCVYASGHPRPDITWAKDDQALTRPEAEFRKKWTLSLKNLRPDSG	21		
DB	2631 --AQP--GNLVOLQCLAHGTPLPLTYQWSLVGVL--PEKAVVRNO--LRLRLEPYVPEDSG	26		
OY	216 KTYCIVSRNAGAIINTYKVDIVQRTSRK-----	PVLGTGHPVNTVDFGTTSE	26	
DB	2683 RYRCVSNRVSAGAEFAQV-LVQSSSSNLPDTSITGSGTPIYQVY-POLETRNIGASVEF	27		
OY	265 QCKVRSDVKPYIQLKRVYEGAEGRHNSITIDYGGQKFVLLPTG	307		
DB	2741 HCAVPNERGTHLRWLKE-----	GGQ---LPPG	2764	
RESULT 20				
PGBM_HUMAN	STANDARD:	PRT:	4393	AA.
ID	PGBM_HUMAN	998160;	016287;	
AC	01-OCT-1996	(Rel. 34,	Created)	
DT	01-OCT-1996	(Rel. 34,	Last sequence update)	
DT	20-AUG-2001	(Rel. 40,	Last annotation update)	
DE	BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE			
DE	PROTEIN PRECURSOR (HSPG) (PERLECAN) (PLC).			
GN	HSPG2.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=92112994;	PubMed=1730768;		
RA	Kallunki P., Tryggvason K.;			
RT	"Human basement membrane heparan sulfate proteoglycan core protein:			
RT	467-kD protein containing multiple domains resembling elements of th			
RT	low density lipoprotein receptor, laminin, neural cell adhesion			
RT	molecules, and epidermal growth factor.";			
RL	J. Cell Biol. 116:559-571(1992).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Skin, and Colon;			
RX	MEDLINE=92235084;	PubMed=1569102;		
RA	Murdoch A.D., Dodge G.R., Cohen I., Tuan R.S., Iozzo R.V.;			
RT	"Primary structure of the human heparan sulfate proteoglycan from			
RT	basement membrane (HSPG/perlecan). A chimeric molecule with multipl			
RT	domains homologous to the low density lipoprotein receptor, laminin,			
RT	neural cell adhesion molecules, and epidermal growth factor.";			
RL	J. Biol. Chem. 267:8544-8557(1992).			
RN	[3]			
RP	SEQUENCE OF 1018-1472 FROM N.A.			
RC	TISSUE=Colon;			
RX	MEDLINE=91365376;	PubMed=1679749;		
RA	Dodge G.R., Kovalszky I., Chu M.L., Hassell J.R., McBride O.W.,			
RA	Yi H.F., Iozzo R.V.;			
RT	"Heparan sulfate proteoglycan of human colon: partial molecular			
RT	cloning, cellular expression, and mapping of the gene (HSPG2) to the			
RT	short arm of human chromosome 1.";			

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RL Genomics 10:673-680(1991).
RN [4]
RP SEQUENCE OF 892-1398 FROM N.A.
RC TISSUE=Fibrosarcoma;
RX MEDLINE=92120660; PubMed=1685141;
RA Kallunki P., Eddy R.L., Byers M.G., Kestila M., Shows T.B.,
RT Tryggvason K.;
RT "Cloning of human heparan sulfate proteoglycan core protein,
RT assignment of the gene (HSPG2) to 1p36.1->p35 and identification of
RT a BamHI restriction fragment length polymorphism.";
RL Genomics 11:389-396(1991).
RN [5]
RP SEQUENCE OF 1-21 FROM N.A.
RX MEDLINE=94052171; PubMed=8234307;
RA Cohen I.R., Graessell S., Murdoch A.D., Iozzo R.V.;
RT "Structural characterization of the complete human perlecan gene and
RT its promoter.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:10404-10408(1993).
CC -1- FUNCTION: THIS PROTEIN IS AN INTEGRAL COMPONENT OF BASEMENT
CC MEMBRANES. IT IS RESPONSIBLE FOR THE FIXED NEGATIVE ELECTROSTATIC
CC CHARGE AND IS INVOLVED IN THE CHARGE-SELECTIVE ULTRAFILTRATION
CC PROPERTIES. IT INTERACTS WITH OTHER BASEMENT MEMBRANE COMPONENTS
CC SUCH AS LAMININ AND COLLAGEN TYPE IV AND SERVES AS AN ATTACHMENT
CC SUBSTRATE FOR CELLS.
CC -1- SUBUNIT: PURIFIED PERLECAN HAS A STRONG TENDENCY TO AGGREGATE IN
CC DIMERS OR SPLEATE STRUCTURES.
CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR.
CC -1- TISSUE SPECIFICITY: FOUND IN THE BASEMENT MEMBRANES.
CC -1- PTM: CONTAINS THREE HEPARAN SULFATE CHAINS AS WELL AS N-LINKED
CC AND O-LINKED OLIGOSACCHARIDES.
CC -1- SIMILARITY: CONTAINS 4 LDL-RECEPTOR CLASS A DOMAINS.
CC -1- SIMILARITY: CONTAINS 10.5 LAMININ EGF-LIKE DOMAINS.
CC -1- SIMILARITY: CONTAINS 3 LAMININ DOMAINS IV.
CC -1- SIMILARITY: CONTAINS 22 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC -1- SIMILARITY: CONTAINS 3 LAMININ G-LIKE DOMAINS.
CC -1- SIMILARITY: CONTAINS 4 EGF-LIKE DOMAINS.
CC -1- SIMILARITY: CONTAINS 1 SEA DOMAIN.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X62515; CAA44373.1; -
DR EMBL: M85289; AAA52700.1; -
DR EMBL: M64283; AAA52699.1; -
DR EMBL: S76436; AAB21121.2; -
DR HSSP: I22078; -; NOT_ANNOTATED_CDS.
DR HSSP: P00740; 11XA.
DR MIM: 142461; -
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR000742; EGF_2.
DR InterPro: IPR001438; EGF_II.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003598; Ig_C2.
DR InterPro: IPR002172; LDL_recept_A.
DR InterPro: IPR000034; Laminin_B.
DR InterPro: IPR002049; Laminin_EGF.
DR InterPro: IPR001791; Laminin_G.
DR InterPro: IPR000082; SEA.
DR Pfam: PF00008; EGF_4.
DR Pfam: PF00047; Ig_22.
DR Pfam: PF00052; Laminin_B_3.
DR Pfam: PF00053; Laminin_EGF_8.
DR Pfam: PF00054; Laminin_G_3.
DR Pfam: PF00057; LDL_recept_a; 4.
DR Pfam: PF01390; SEA_1.
DR PRINTS: PR00010; EGFBLDOD.
DR ProDom: PD003031; Laminin_B_3.
DR SMART; SM00180; EGF_Lam; 6.

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DR SMART; SM00001; EGF-like; 8.
DR SMART; SM00408; IGC2; 22.
DR SMART; SM00281; Lamb; 3.
DR SMART; SM00282; Lamb; 3.
DR SMART; SM00192; LDla; 4.
DR SMART; SM00200; SEA; 1.
DR PROSITE; PS00022; EGF_1; 9.
DR PROSITE; PS01186; EGF_2; 5.
DR PROSITE; PS01248; LAMININ_TYPE_EGF; 11.
DR PROSITE; PS01209; LDLRA_1; 4.
DR PROSITE; PS50068; LDLRA_2; 4.
DR PROSITE; PS50024; SEA; 1.
DR SIGNAL; Basement membrane; Proteoglycan; Repeat; Glycoprotein;
DR Heparan sulfate; Laminin EGF-like domain; Immunoglobulin domain;
KW Extracellular matrix; EGF-like domain.
FT SIGNAL 1 21
FT CHAIN 22 4393
FT FT 80 194
FT DOMAIN 197 236
FT FT 283 321
FT DOMAIN 323 361
FT FT 366 405
FT DOMAIN 405 506
FT FT 523 532
FT DOMAIN 533 732
FT FT 733 765
FT DOMAIN 766 815
FT FT 816 815
FT DOMAIN 816 873
FT FT 881 925
FT DOMAIN 926 935
FT FT 936 1127
FT DOMAIN 1128 1160
FT FT 1161 1210
FT DOMAIN 1211 1267
FT FT 1277 1326
FT DOMAIN 1327 1336
FT FT 1337 1531
FT DOMAIN 1532 1564
FT FT 1565 1614
FT DOMAIN 1615 1672
FT FT 1679 1773
FT DOMAIN 1774 1867
FT FT 1868 1957
FT DOMAIN 1958 2054
FT FT 2054 2153
FT DOMAIN 2154 2246
FT FT 2247 2342
FT DOMAIN 2343 2438
FT FT 2439 2535
FT DOMAIN 2536 2631
FT FT 2632 2728
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FT DOMAIN 3115 3213
FT FT 3214 3300
FT DOMAIN 3301 3401
FT FT 3402 3490
FT DOMAIN 3491 3576
FT FT 3577 3671
FT DOMAIN 3671 3847
FT FT 3847 3883
FT DOMAIN 3886 3924
FT FT 3924 3965
FT DOMAIN 3966 4104
FT FT 4106 4143
FT DOMAIN 4145 4178
FT FT 4243 4391
FT SITE 65 67
FT SITE 71 73
FT SITE 76 78
FT SITE 4151 4153

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BASEMENT MEMBRANE-SPECIFIC HEPARAN
SULFATE PROTEOGLYCAN CORE PROTEIN.
SEA.
LDL-RECEPTOR CLASS A 1.
LDL-RECEPTOR CLASS A 2.
LDL-RECEPTOR CLASS A 3.
LDL-RECEPTOR CLASS A 4.
IG-LIKE C2-TYPE DOMAIN 1.
LAMININ EGF-LIKE 1 (N-TERMINAL).
LAMININ EGF-LIKE 1 (C-TERMINAL).
LAMININ EGF-LIKE 2.
LAMININ EGF-LIKE 3.
LAMININ EGF-LIKE 4 (INCOMPLETE).
LAMININ EGF-LIKE 5 (N-TERMINAL).
LAMININ EGF-LIKE 5 (C-TERMINAL).
LAMININ EGF-LIKE 6.
LAMININ EGF-LIKE 7.
LAMININ EGF-LIKE 8.
LAMININ EGF-LIKE 9 (N-TERMINAL).
LAMININ EGF-LIKE 9 (C-TERMINAL).
LAMININ EGF-LIKE 10.
LAMININ EGF-LIKE 11.
IG-LIKE C2-TYPE DOMAIN 2.
IG-LIKE C2-TYPE DOMAIN 3.
IG-LIKE C2-TYPE DOMAIN 4.
IG-LIKE C2-TYPE DOMAIN 5.
IG-LIKE C2-TYPE DOMAIN 6.
IG-LIKE C2-TYPE DOMAIN 7.
IG-LIKE C2-TYPE DOMAIN 8.
IG-LIKE C2-TYPE DOMAIN 9.
IG-LIKE C2-TYPE DOMAIN 10.
IG-LIKE C2-TYPE DOMAIN 11.
IG-LIKE C2-TYPE DOMAIN 12.
IG-LIKE C2-TYPE DOMAIN 13.
IG-LIKE C2-TYPE DOMAIN 14.
IG-LIKE C2-TYPE DOMAIN 15.
IG-LIKE C2-TYPE DOMAIN 16.
IG-LIKE C2-TYPE DOMAIN 17.
IG-LIKE C2-TYPE DOMAIN 18.
IG-LIKE C2-TYPE DOMAIN 19.
IG-LIKE C2-TYPE DOMAIN 20.
IG-LIKE C2-TYPE DOMAIN 21.
IG-LIKE C2-TYPE DOMAIN 22.
LAMININ G-LIKE 1 (GLOBULAR DOMAIN V A).
EGF-LIKE 2.
LAMININ G-LIKE 2 (GLOBULAR DOMAIN V B).
EGF-LIKE 3.
LAMININ G-LIKE 3 (GLOBULAR DOMAIN V C).
HEPARAN SULFATE (POTENTIAL).
HEPARAN SULFATE (POTENTIAL).
HEPARAN SULFATE (POTENTIAL).
MEDIATES MOTOR NEURON ATTACHMENT

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FT	SITE	4301	4303	(POTENTIAL) MEDIATES MOTOR NEURON ATTACHMENT (POTENTIAL).
FT	DISULFID	199	212	BY SIMILARITY.
FT	DISULFID	206	225	BY SIMILARITY.
FT	DISULFID	219	234	BY SIMILARITY.
FT	DISULFID	285	297	BY SIMILARITY.
FT	DISULFID	292	310	BY SIMILARITY.
FT	DISULFID	304	319	BY SIMILARITY.
FT	DISULFID	325	337	BY SIMILARITY.
FT	DISULFID	332	350	BY SIMILARITY.
FT	DISULFID	344	359	BY SIMILARITY.
FT	DISULFID	368	381	BY SIMILARITY.
FT	DISULFID	375	394	BY SIMILARITY.
Query Match	Best Local Similarity	12.5%;	Score 222.5;	DB 1; Length 4393;
Matches	63; Conservative	33;	Mismatches	75; Indels 51; Gaps 8;
53	GDPPEPTMTKDGRTTHSGMSRFRVLPGQ--LKQVEREDAGVYCKATNGFSLSNVY	110		
Db	3516	GDPKQYTWKSVGKHLRPG-----IVQSGGVRIAHVELADAGQYCTATNNAQTQSHV	3570	
Qy	111	TLVYVLDLDSPEKESLGFDSSGGEDEPQASQARPRFTQPSKRRVVIARPPVGSVRLKC	170	
Db	3571	LLLV-----QALPQISMGEVR-----VPAGSAAVFPC	3598	
Qy	171	VASGHPRDITAMKDDOALTRPEAEPRKKKWTLSLKNLPEDSGKYTCRVSRAQAINA	230	
Db	3559	IASGTPPDIDSMKSLDLSL-----PPDSRLNNMLMLPVOPODAGTYCTATNRQCKVNA	3654	
Qy	231	TYKVDVIGRTSRKPEVLGTGTH---PVNTVDFGSGTSPQCKV	268	
Db	3655	FAHQLQVERV--VYFTQTPYSFLPPTLTD--AYRKFEKI	3692	
RESULT	21			
FGRL_DROME	STANDARD;	PRT;	730	AA.
AC	007407;			
DT	01-NOV-1995 (Rel. 32, Created)			
DT	01-NOV-1995 (Rel. 32, Last sequence update)			
DT	20-AUG-2001 (Rel. 40, Last annotation update)			
DE	FIBROBLAST GROWTH FACTOR RECEPTOR HOMOLOG 1 PRECURSOR (EC 2.7.1.112)			
DE	(HEARTLESS PROTEIN).			
DE	FRI OR HTL OR DTKL.			
S	Drosophila melanogaster (Fruit fly).			
S	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;			
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;			
OC	Ephydroidea; Drosophilidae; Drosophila.			
OX	NCBI_Taxid=7227;			
RN	[1]			
RE	SEQUENCE FROM N.A.			
RC	TISSUE=Embryo;			
RA	MEDLINE=94156202; PubMed=8112607;			
RA	Ito M., Matsui T., Taniguchi T., Chihara K.;			
RT	"Alternative splicing generates two distinct transcripts for the			
RT	Drosophila melanogaster fibroblast growth factor receptor homolog.";			
RL	Gene 139:215-218(1994).			
RN	[2]			
RN	SEQUENCE FROM N.A.			
RP	STRAIN=CANTON-S;			
RX	MEDLINE=93321617; PubMed=8330538;			
RA	Shishido E., Higashijima S.-I., Emori Y., Saigo K.;			
RT	"Two FGF-receptor homologues of Drosophila: one is expressed in			
RT	mesodermal primordium in early embryos.";			
RL	Development 117:751-761(1993).			
CC	-1- FUNCTION: MAY BE REQUIRED FOR PATTERNING OF MUSCLE PRECURSOR			
CC	CELLS. WOULD THUS APPEAR ESSENTIAL FOR GENERATION OF MESODERMAL			
CC	AND ENDODERMAL LAYERS. INVAGINATIONS OF VARIOUS TYPES OF CELLS,			
CC	AND CNS FORMATION.			
CC	-1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + PROTEIN			
CC	TYROSINE PHOSPHATE.			
CC	-1- SUBCELLULAR LOCATION: TYPE 1 MEMBRANE PROTEIN.			
CC	-1- TISSUE SPECIFICITY: MESODERM.			
CC	-1- DEVELOPMENTAL STAGE: EMBRYOGENESIS.			
CC	-1- SIMILARITY: BELONGS TO THE FIBROBLAST GROWTH FACTOR RECEPTOR			
CC	FAMILY.			
CC	-1- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.			
CC	-1- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-16 IS THE INITIATOR.			
CC	CC			
CC	EMBL: D14976; BAA03616.1; -			
CC	EMBL: D14977; BAA03617.1; -			
CC	EMBL: X74030; CAA52189.1; -			
CC	HSSP: P11362; IEG1.			
CC	DR FlyBase: FBgn0010389; htl.			
CC	DR InterPro: IPR000719; Euk.pkinase.			
CC	DR InterPro: IPR003066; Ig.MHC.			
CC	DR InterPro: IPR003598; Ig.C2.			
CC	DR InterPro: IPR003600; Ig.Like.			
CC	DR InterPro: IPR001245; Tyr_kin.			
CC	DR Pfam: PF00047; Ig_1.			
CC	DR Pfam: PF00069; pkinase.1.			
CC	DR PRINTS: PR00109; TYRKINASE.			
CC	DR SMART: SM00408; IGC2; 1.			
CC	DR SMART: SM00410; IG_Like; 1.			
CC	DR SMART: SM00219; TYRK; 1.			
CC	DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.			
CC	DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.			
CC	DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.			
CC	KW Receptor; Glycoprotein; Tyrosine-protein kinase; ATP-binding;			
CC	KW Transferrase; Phosphorylation; Transmembrane; Immunoglobulin domain;			

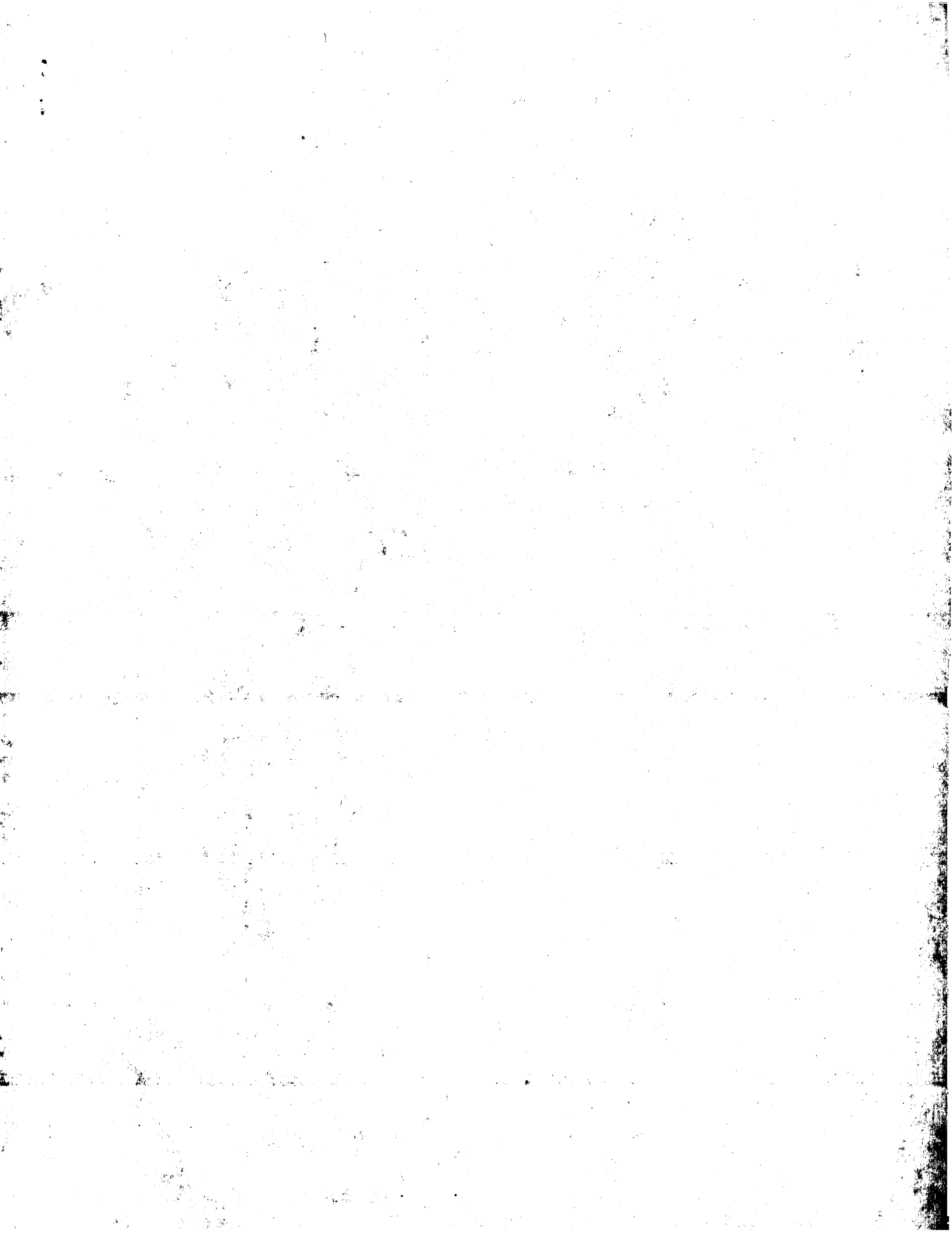












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OM protein - protein search, using sw model

Run on: May 2, 2002, 08:47:43 : Search time 24.18 seconds  
(Without alignments)  
986.419 Million cell updates/sec

Title: US-09-823-038a-33

Perfect score: 1779

Sequence: 1 RRAPCCCSCRCRCWGPMSHR.....VLPTGDVMSRPDGYLNKPL 322

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Listing first 100 summaries

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22: /SIDSR/gcgdata/geneseq/geneseq/AA2001.DAT:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Length	ID	Description
1	1779	100.0	322	AA19116
2	1448	81.4	504	AA19116
3	1448	81.4	504	AA19116
4	1448	81.4	504	AA19116
5	1448	81.4	504	AA19116
6	1448	81.4	504	AA19116
7	1448	81.4	504	AA19116
8	1371	77.1	529	AA19116
9	1029	57.8	439	AA19116
10	1019	57.3	365	AA19116
11	1019	57.3	371	AA19116

12	529	29.7	101	AA19116
13	383	21.5	389	AA19116
14	378	21.2	561	AA19116
15	375.5	21.1	355	AA19116
16	375.5	21.1	643	AA19116
17	373	21.0	816	AA19116
18	371.5	20.9	769	AA19116
19	371.5	20.9	821	AA19116
20	365.5	20.5	820	AA19116
21	364.5	20.5	622	AA19116
22	364.5	20.5	820	AA19116
23	364.5	20.5	820	AA19116
24	364.5	20.5	822	AA19116
25	360.5	20.3	351	AA19116
26	360.5	20.3	822	AA19116
27	360.5	20.3	822	AA19116
28	360.5	20.3	822	AA19116
29	358.5	20.2	819	AA19116
30	350	19.7	126	AA19116
31	349.5	19.6	820	AA19116
32	348	19.6	764	AA19116
33	318	17.9	679	AA19116
34	308	17.3	472	AA19116
35	308	17.3	472	AA19116
36	308	17.3	472	AA19116
37	308	17.3	472	AA19116
38	308	17.3	472	AA19116
39	308	17.3	472	AA19116
40	308	17.3	525	AA19116
41	308	17.3	525	AA19116
42	308	17.3	731	AA19116
43	307	17.3	240	AA19116
44	307	17.3	263	AA19116
45	307	17.3	304	AA19116
46	307	17.3	526	AA19116
47	307	17.3	652	AA19116
48	307	17.3	726	AA19116
49	307	17.3	787	AA19116
50	304	17.1	287	AA19116
51	303	17.0	731	AA19116
52	299	16.8	488	AA19116
53	299	16.8	497	AA19116
54	299	16.8	497	AA19116
55	295	16.6	211	AA19116
56	292.5	16.4	750	AA19116
57	283.5	15.9	729	AA19116
58	282.5	15.9	729	AA19116
59	282.5	15.9	729	AA19116
60	282.5	15.9	731	AA19116
61	241.5	13.6	753	AA19116
62	237	13.3	1649	AA19116
63	237	13.3	1651	AA19116
64	237	13.3	2387	AA19116
65	237	13.3	2597	AA19116
66	235	13.2	767	AA19116
67	234.5	13.2	1101	AA19116
68	233	13.1	1297	AA19116
69	233	13.1	1297	AA19116
70	233	13.1	1395	AA19116
71	233	13.1	1395	AA19116
72	232.5	13.1	3117	AA19116
73	230	12.9	1496	AA19116
74	230	12.9	1496	AA19116
75	229	12.9	1853	AA19116
76	228	12.8	1380	AA19116
77	228	12.8	1381	AA19116
78	222.5	12.5	4393	AA19116
79	217.5	12.2	22	AA19116
80	214	12.0	467	AA19116
81	213.5	12.0	1242	AA19116
82	213	12.0	1059	AA19116
83	213	12.0	1059	AA19116
84	213	12.0	1059	AA19116

Human prostate can	Angiotensin conver	Extracellular doma	Clone pPB1229-enco	Human fibroblast g	Clone pPB1284-enco	flg receptor prote	Fibroblast growth	Human FGF-R1 Extra	Human fibroblast g	Amino acid sequenc	Mouse fibroblast g	FGFR 1 (flg 5) ext	Basic FGF receptor	flg receptor prote	N-sam. Homo sapie	Chicken basic fibr	Polypeptide isolat	Mouse bFGF recepto	Lung cancer associ	K-sam. Homo sapie	Fibroblast growth	Human FGF-R1-tpa fu	Human FGF-R1-tpa fu	Human FGF-R1-tpa fu	Human FGF-R1-tpa fu	Human FGF-R1 Extra	Human bFGF recept	Extracellular doma	Rat FGF-R1. Ratu	Rat FGF-R1. flagged	Clone pPB1283-enco	KGF receptor. Mus	Murine KGF recepto	Human FGF-R1. Hom	Chicken basic fibr	Human FGF-R1 Extra	Human FGF-R1 Extra	Human FGF-R1 Extra	D2-D3 region of hu	D2-D3 region of hu	Keratinocyte growt	Fibroblast growth	Newt keratinocyte	Human r65 protein.	Human R601 protei	Human Robo 1 polyp	Mechanical stress	Human protein sequ	Human H1G-1 prote	C. elegans Robo po	Drosophila Robo 1	Drosophila sp. Rob	Sequence g1/332818	Melanoma associat	Human p53 target m	protein 608 sequen	Drosophila sp. Rob	Amino acid sequenc	FGFR 1 (flg 5) ext	Nsk2 receptor with	Rattus norvegicus	Human PBO335 prote	Amino acid sequenc	Human PBO335 prote
--------------------	--------------------	--------------------	--------------------	--------------------	--------------------	--------------------	-------------------	--------------------	--------------------	--------------------	--------------------	--------------------	--------------------	--------------------	-------------------	--------------------	--------------------	--------------------	--------------------	-------------------	-------------------	---------------------	---------------------	---------------------	---------------------	--------------------	-------------------	--------------------	------------------	---------------------	--------------------	-------------------	--------------------	-------------------	--------------------	--------------------	--------------------	--------------------	--------------------	--------------------	--------------------	-------------------	-------------------	--------------------	-------------------	--------------------	-------------------	--------------------	-------------------	--------------------	-------------------	--------------------	--------------------	-------------------	--------------------	--------------------	--------------------	--------------------	--------------------	--------------------	-------------------	--------------------	--------------------	--------------------

85	213	12.0	1059	22	AAU00825	Human immune respo
86	213	12.0	1059	22	AAB80261	Human PRO335 prote
87	213	12.0	1119	20	AAU08114	Human PRO326 prote
88	213	12.0	1119	21	AAU08114	Human PRO326 prote
89	213	12.0	1119	22	AAU12347	Human PRO326 polyp
90	213	12.0	1119	22	AAU00827	Human immune respo
91	213	12.0	1119	22	AAB80263	Human PRO326 prote
92	213	12.0	1119	22	AAB8162	Human PRO326 polyp
93	212.5	11.9	739	22	AAB62398	Human MBSP2 polype
94	210.5	11.8	791	20	AAU08096	Murine glial cell
95	210.5	11.8	825	20	AAU08115	Murine glial cell
96	210.5	11.8	1081	18	AAU41641	Sequence used in d
97	210.5	11.8	1091	20	AAU08099	Murine glial cell
98	210.5	11.8	1091	20	AAU08010	Mouse Lig-1 protei
99	210.5	11.8	1091	21	AAU97833	Murine Lig-1 prote
100	208.5	11.7	932	22	AAE05252	Mouse Nope (neighb

## ALIGNMENTS

## RESULT 1

ID AAB19116 standard; Protein; 322 AA.

AC AAB19116;

DT 19-FEB-2001 (first entry)

DE Homologue of polypeptide from lymph node stromal cells of fsn -/- mice.

KW Lymph node stromal cell; fsn -/- mice; inflammatory disorder;

KW immune system disorder; cancer; viral infection; HIV infection;

KW blood vessel growth; tumour necrosis factor disorder; arthritis;

KW inflammatory bowel disease; fibroblast growth factor-mediated disorder;

KW cardiac failure.

KW Homo sapiens.

KW WO200058463-A1.

PD 05-OCT-2000.

PF 18-FEB-2000; 2000WO-NZ00015.

PR 25-MAR-1999; 99US-0276268.

PR 26-AUG-1999; 99US-0383586.

XX (GENE-) GENESIS RES &amp; DEV CORP LTD.

XX Strachan L, Sleeman M, Abernethy N, Onrust R, Kumble KD;

XX Murison JG;

XX MPI: 2000-664924/64.

XX N-PSDB; AAA96726.

XX Polypeptide expressed in mammalian fsn -/- lymph node stromal cells,

XX useful for modulating growth of blood cells, for treating inflammatory

XX disorders -

XX Claim 1; Page 53-54; 75pp; English.

XX The present sequence represents a homologue of a polypeptide sequence

XX which is isolated from lymph node stromal cells of fsn -/- mice. The

XX inflammatory disorder, and their polypeptides are useful for treating an

XX inflammatory disorder, disorder of immune system and cancer selected

XX from epithelial, lymphoid, myeloid, stromal and neuronal cancers, a

XX viral disorder, in particular HIV infection and for modulating the

XX growth of blood vessels. The polypeptides are useful for treating a

XX tumour necrosis factor (TNF) mediated disorder, such as those selected

XX from arthritis, inflammatory bowel disease and cardiac failure and a

XX fibroblast growth factor-mediated disorder. It is also useful in assays

to determine biological activity, to raise antibodies, to isolate corresponding ligands or receptors, to quantify levels of protein or cognate corresponding ligand or receptors, as anti-inflammatory agents, and in compositions for the treatment of skin, connective tissue and immune system diseases. The polynucleotide is useful as marker for tissue, as a chromosome marker or tags in the identification of a genetic disorder.

SQ Sequence 322 AA;

Query Match 100.0%; Score 1779; DB 21; Length 322;

Best Local Similarity 100.0%; Pred. No. 3,6e-122;

Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRAPCCSCCRRCRCGSHRPPPEAPQRRRTWSHGRRPAGCHCAAPVEGDPPLTM 60

DB 1 RRAPCCSCCRRCRCGSHRPPPEAPQRRRTWSHGRRPAGCHCAAPVEGDPPLTM 60

QY 61 WTKDGRTHSGSRFRVLPGLKVKOVERDAGVYCKATNGSGLSVNTVTLVLDISP 120

DB 61 WTKDGRTHSGSRFRVLPGLKVKOVERDAGVYCKATNGSGLSVNTVTLVLDISP 120

QY 121 GKESLGPDSSSSGQEDPASQOMARPRFTOPSKRRRRVIRAPVSSVRLKCVASGHRPDI 180

DB 121 GKESLGPDSSSSGQEDPASQOMARPRFTOPSKRRRRVIRAPVSSVRLKCVASGHRPDI 180

QY 181 TWMKDQALTRPPAAPRRKKKTLKLNLRPDSGTYTCVSRACAINATYKVVDYQRT 240

DB 181 TWMKDQALTRPPAAPRRKKKTLKLNLRPDSGTYTCVSRACAINATYKVVDYQRT 240

QY 241 RSKPVLTHGHPVNTVDFGTTSFQCKVRSQVYPIVOMLRVYGEGRHNSRTIDVGQK 300

DB 241 RSKPVLTHGHPVNTVDFGTTSFQCKVRSQVYPIVOMLRVYGEGRHNSRTIDVGQK 300

QY 301 FVVLPTGVDVMSRPDGSYLKPKL 322

DB 301 FVVLPTGVDVMSRPDGSYLKPKL 322

## RESULT 2

ID AAB24066 standard; Protein; 504 AA.

AC AAB24066;

DT 29-JAN-2001 (first entry)

DE Human PRO943 protein sequence SEQ ID NO:29.

KW Human; tumour; diagnosis; neoplastic disease; neoplastic cell growth;

KW proliferation; tumourigenesis; identification; cancer; cytostatic;

KW neurotropic; neuroprotective; anti-inflammatory; immunosuppressive;

KW immunostimulant; antiangiogenic; leukaemia; lymphoid malignancy;

KW neuronal disorder; glial disorder; astrocytal disorder; angiogenic;

KW hypothalamic disorder; glandular disorder; macropagal disorder;

KW epithelial disorder; stromal disorder; blastocoele disorder;

KW inflammatory disorder; immunologic disorder.

KW Homo sapiens.

KW WO200053755-A2.

PD 14-SEP-2000.

PF 06-JAN-2000; 2000WO-US00376.

PR 08-MAR-1999; 99WO-US05028.

PR 02-JUN-1999; 99WO-US12252.

PR 23-JUN-1999; 99US-0141037.

PR 07-JUL-1999; 99US-0143048.

PR 26-OUL-1999; 99US-0145698.

PR 30-NOV-1999; 99WO-US28313.









DE Human PRO943 (UNQ480) protein sequence SEQ ID NO:119.  
 XX  
 XX Human: secreted and transmembrane protein: PRO: cytostatic:  
 KW cell death: cancer: chromosomal mapping; gene mapping; tissue typing;  
 KW diagnostic assay.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200073454-A1.  
 XX  
 PD 07-DEC-2000.  
 XX  
 XX 30-MAR-2000; 2000WO-US08439.  
 XX  
 XX 02-JUN-1999; 99WO-US12252.  
 PR 23-JUN-1999; 99US-0141037.  
 PR 07-JUL-1999; 99US-0143048.  
 PR 20-JUL-1999; 99US-0144758.  
 PR 26-JUL-1999; 99US-0145698.  
 PR 28-JUL-1999; 99US-0146222.  
 PR 17-AUG-1999; 99US-0149396.  
 PR 15-SEP-1999; 99WO-US21090.  
 PR 08-OCT-1999; 99WO-US21547.  
 PR 30-NOV-1999; 99US-0158663.  
 PR 01-DEC-1999; 99WO-US28301.  
 PR 16-DEC-1999; 99WO-US30095.  
 PR 20-DEC-1999; 99WO-US30911.  
 PR 05-JAN-2000; 2000WO-US00219.  
 PR 06-JAN-2000; 2000WO-US00376.  
 PR 11-FEB-2000; 2000WO-US03565.  
 PR 18-FEB-2000; 2000WO-US04341.  
 PR 22-FEB-2000; 2000WO-US04414.  
 PR 24-FEB-2000; 2000WO-US04914.  
 PR 24-FEB-2000; 2000WO-US05004.  
 PR 15-MAR-2000; 2000WO-US05841.  
 PR 20-MAR-2000; 2000WO-US07377.  
 XX  
 XX (GETH ) GENENTECH INC.  
 XX  
 PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;  
 PI Ferrara N, Fong S, Gether H, Gertlisen ME, Goddard A, Gadowski PJ;  
 PI Grimaldi CJ, Gurney AL, Kijavlin IJ, Napier MA, Pan J, Pasoni NF;  
 PI Roy MA, Stewart JA, Tumas D, Watanabe CK, Williams PM, Wood WI;  
 PI Zhang Z;  
 XX  
 DR WPI: 2001-032160/04.  
 DR N-PSDB; AAF44130.  
 XX  
 PT PRO polynucleotides used to produce polypeptides used to target  
 PT bioactive molecules such as toxins, radiolabels or antibodies, to  
 PT specific cells, to cause targeted cell death -  
 XX  
 PS Claim 12; Fig 70; 935pp; English.  
 XX  
 CC The present invention describes human secreted and transmembrane PRO  
 CC proteins. The PRO proteins have cytostatic activity. The PRO proteins  
 CC can be used for targeted delivery of bioactive molecules, such as  
 CC toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide  
 CC sequences, and their fragments, can be used as hybridisation probes, in  
 CC chromosomal and gene mapping, and in the generation of anti-sense RNA  
 CC and DNA. They may also be used to produce transgenic animals which are  
 CC used to develop and screen therapeutically useful reagents. The PRO  
 CC nucleotide and protein sequence can be used for tissue typing and in  
 CC treating cancer. Anti-PRO antibodies can be used in diagnostic assays.  
 CC AAF44270 to AAF44470 represent PCR primers and hybridisation probes  
 CC in the isolation of human PRO sequences. AAF44087 to AAF44269 and  
 CC AAB55154 to AAB55300 represent human PRO polynucleotide and protein  
 CC sequences given in the exemplification of the present invention.  
 XX  
 SO Sequence 504 AA:

Query Match 81.4%; Score 1448; DB 22; Length 504;  
 Best Local Similarity 99.6%; Pred. No. 7.9e-98;  
 Matches 212; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 50 PVEGDPPPLTMMTKDGRRTISGMSRFRVLPOGLKVKOVEREDAGVYCKATNGFGSLVN 109  
 DB 52 pvegdppplmmwtkdgrtlisgmsrfrvlpqglkvkqveredagvyckatngfslvn 111  
 QY 110 YTLVLDLIDISPKRESLIGDSSSGQEDPASQOMARPRPTOPSKMRRVIAAPGVSSVRLK 169  
 DB 112 ytlvldldispgkresligrdsssgqedpasqwarprftgskmrrviarpvssvrlk 171  
 QY 170 CVASGHRPDLTMMKDDOALTRPEAAPERRKKMTLSIKNLRPDSGCTYTORVSNRAIN 229  
 DB 172 cvasghrpdlmmkddqaltrpeaaeprrkkwclsknlrpdsgkytcorvsnraain 231  
 QY 230 ATYKVDVLTQRTSRKPVLTGTHPVNTTVDGFTTSFOCKVSDVKPVLTMLKRYEGAGGR 289  
 DB 232 atykvdvltqtrskpvlgtghpvnntvdfgfttsfgckvsvdkpvltmlykryegaegr 291  
 QY 290 HNSTIDVGGKFPVLPFGDWSRPPDSYLNKPL 322  
 DB 292 hnstldvggkfpvlpgdwsrpdsgsylnkpl 324  
 RESULT 6  
 AAB66264  
 ID AAB66264 standard; Protein; 504 AA.  
 XX  
 AC AAB66264;  
 XX  
 DT 05-APR-2001 (first entry)  
 XX  
 DE Human MANGO 003 SEQ ID NO: 5.  
 XX  
 XX Membrane associated protein; secreted protein; human; mouse; rat;  
 KW INTERCEPT 340; MANGO 003; MANGO 347; TANGO 272; TANGO 295; TANGO 354;  
 KW TANGO 378; skeletal disorder; cardiovascular disorder; renal disorder;  
 KW haematopoietic disorder; neural disorder; hepatic disorder;  
 KW neoplastic disease.  
 XX  
 OS Homo sapiens.  
 OS  
 OS  
 PN WO200100673-A1.  
 XX  
 PD 04-JAN-2001.  
 XX  
 PF 29-JUN-2000; 2000WO-US18198.  
 XX  
 PR 30-JUN-1999; 99US-0345464.  
 XX  
 PA (MILL-) MILLENNIUM PHARM INC.  
 XX  
 PI Barnes TM, Fraser CC, Wighton N, Myers P, Busfield SJ, Sharp JD;  
 PI WPI: 2001-050128/06.  
 DR N-PSDB; AAF27781.  
 XX  
 PT Isolated secreted or transmembrane proteins are used for diagnosis and  
 PT treatment of neoplastic and haematopoietic disorders e.g. T cell  
 PT disorders, cancer and tumours -  
 XX  
 PS Claim 9; Page 216-217; 294pp; English.  
 XX  
 CC The present invention provides the protein and coding sequences for a  
 CC number of membrane associated and secreted proteins from human, mouse and  
 CC rat. The proteins are designated INTERCEPT 340, MANGO 003, MANGO 347,  
 CC TANGO 272, TANGO 295, TANGO 254 and TANGO 378. The proteins are all  
 CC involved in signal transduction and the sequences can be used in the  
 CC treatment of cardiovascular, renal, hepatic, neural, neoplastic, skeletal  
 CC and haematopoietic disorders.

SQ Sequence 504 AA;

Query Match 81.4%; Score 1448; DB 22; Length 504;  
 Best Local Similarity 99.6%; Pred. No. 7.9e-98;  
 Matches 272; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 50 PVEGDPPPLTMMTKDGRTHSGMSRFRVLPQGLKVKYQVERDAGYVCATNGFGLSVN 109  
 |||  
 Db 52 pvegdpppltmwtkdgrthshgwsfrvlpqglkvkyqverdagyyvckatngfglsvn 111  
 QY 110 YTLVVLDDISPGKESLGPDSGGQEDPASQOMARPRFTOPSKMRRYIARPVGSSVRLK 169  
 |||  
 Db 112 ytlvvladdispgkeslgpdsagggedpasqgwarprftgskmrryiarpvgsavrlk 171  
 QY 170 CVASGHPRPDITWMKDDQALTRPEAEPRKKRWLTLKLNLRPEDSGKYTCRVSNRAGAIN 229  
 |||  
 Db 172 cvasghprpdltmkddqaltrpeaeprkkwllslnlrpedsgkytcrvsnragn 231  
 QY 230 ATYKVDVIQRTSRKPVLTGTHPVNTVDFGCTSPQCKVRSQVDPVLTQMLKRVEXGAGGR 289  
 |||  
 Db 232 atykvvdvigrtrskpvlgtchpntlvdfgctsfqckvrsdvkpvltqwlkrveygaegr 291  
 QY 290 HNSTIDVGQKFFVLPTEGDVWSRPDGSYLKNPL 322  
 |||  
 Db 292 hnstidvggkfvlptegdvwsrpdgsylnkl 324

RESULT 7

AAM38643 ID AAM38643 standard; Protein: 608 AA.

AC AAM38643;

XX 22-OCT-2001 (first entry)

XX Human polypeptide SEQ ID NO 1788.

XX Human: noctropic; immunosuppressant; cytosstatic; gene therapy; cancer;  
 KW peripheral nervous system; neuropathy; central nervous system; CNS;  
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;  
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;  
 KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;  
 KW leukaemia.

XX Homo sapiens.

XX MO200153312-A1.

XX 26-JUL-2001.

XX 26-DEC-2000; 2000WO-US34263.

XX 21-JAN-2000; 2000US-0488725.

XX 25-APR-2000; 2000US-0552317.

XX 09-JUL-2000; 2000US-0598042.

XX 19-JUL-2000; 2000US-0620312.

XX 03-AUG-2000; 2000US-0653450.

XX 14-SEP-2000; 2000US-0662191.

XX 19-OCT-2000; 2000US-0693036.

XX 29-NOV-2000; 2000US-0727344.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;  
 PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;  
 PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;  
 XX WPI: 2001-442253/47.  
 DR N-PSDB; AA157799.  
 XX Novel nucleic acids and polypeptides, useful for treating disorders  
 PT such as central nervous system injuries -

XX Example 3; SEQ ID NO 1788; 10078pp; English.

CC The invention relates to human nucleic acids (AA157798-AA161369) and  
 CC the encoded polypeptides (AAM38642-AAM42213) with noctropic,  
 CC immunosuppressant and cytosstatic activity. The polynucleotides are useful  
 CC in gene therapy. A composition containing a polypeptide or polynucleotide  
 CC of the invention may be used to treat diseases of the peripheral nervous  
 CC system, such as peripheral nervous injuries, peripheral neuropathy and  
 CC localised neuropathies and central nervous system diseases, such as  
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic  
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the  
 CC utilisation of the activities such as: Immune system suppression,  
 CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic  
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,  
 CC assays for receptor activity, arthritis and inflammation, leukaemias and  
 CC C.N.S disorders.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification.

SQ Sequence 608 AA;

Query Match 81.4%; Score 1448; DB 22; Length 608;  
 Best Local Similarity 99.6%; Pred. No. 9.6e-98;  
 Matches 272; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 50 PVEGDPPPLTMMTKDGRTHSGMSRFRVLPQGLKVKYQVERDAGYVCATNGFGLSVN 109  
 |||  
 Db 39 pvegdpppltmwtkdgrthshgwsfrvlpqglkvkyqverdagyyvckatngfglsvn 98  
 QY 110 YTLVVLDDISPGKESLGPDSGGQEDPASQOMARPRFTOPSKMRRYIARPVGSSVRLK 169  
 |||  
 Db 99 ytlvvladdispgkeslgpdsagggedpasqgwarprftgskmrryiarpvgsavrlk 158  
 QY 170 CVASGHPRPDITWMKDDQALTRPEAEPRKKRWLTLKLNLRPEDSGKYTCRVSNRAGAIN 229  
 |||  
 Db 159 cvasghprpdltmkddqaltrpeaeprkkwllslnlrpedsgkytcrvsnragn 218  
 QY 230 ATYKVDVIQRTSRKPVLTGTHPVNTVDFGCTSPQCKVRSQVDPVLTQMLKRVEXGAGGR 289  
 |||  
 Db 219 atykvvdvigrtrskpvlgtchpntlvdfgctsfqckvrsdvkpvltqwlkrveygaegr 278  
 QY 290 HNSTIDVGQKFFVLPTEGDVWSRPDGSYLKNPL 322  
 |||  
 Db 279 hnstidvggkfvlptegdvwsrpdgsylnkl 311

RESULT 8

AAB19114 ID AAB19114 standard; Protein: 529 AA.

AC AAB19114;

XX 19-FEB-2001 (first entry)

XX Polypeptide isolated from lymph node stromal cells of fsn -/- mice.

XX Lymph node stromal cell; fsn -/- mice; inflammatory disorder;  
 KW immune system disorder; cancer; viral infection; HIV infection;  
 KW blood vessel growth; tumour necrosis factor disorder; arthritis;  
 KW inflammatory bowel disease; fibroblast growth factor-mediated disorder;  
 KW cardiac failure.

XX Mus sp.

XX MO200058463-A1.

XX 05-OCT-2000.

XX 18-FEB-2000; 2000WO-NZ00015.

XX 25-MAR-1999; 99US-0276268.

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PR 26-AUG-1999; 99US-0383586.
XX (GENE-) GENESIS RES & DEV CORP LTD.
XX Strachan L, Sleeman M, Abernethy N, Onrust R, Kumble KD;
PI Morrison JG;
XX WPI: 2000-664924/64.
XX N-PSDB; AAA96724.
DR
XX
XX Polypeptide expressed in mammalian fsn -/- lymph node stromal cells,
PT useful for modulating growth of blood cells, for treating inflammatory
PT and tumour necrosis factor-mediated disorders, cancer and viral
PT disorders
XX
XX Claim 1; Page 51-52; 75pp; English.
XX
XX The present sequence represents a polypeptide sequence which is
CC isolated from lymph node stromal cells of fsn -/- mice. The
CC polynucleotides and their polypeptides are useful for treating an
CC inflammatory disorder, disorder of immune system and cancer selected
CC from epithelial, lymphoid, myeloid, stromal and neuronal cancers, a
CC viral disorder, in particular HIV infection and for modulating the
CC growth of blood vessels. The polypeptides are useful for treating a
CC tumour necrosis factor (TNF) mediated disorder, such as those selected
CC from arthritis, inflammatory bowel disease and cardiac failure and a
CC fibroblast growth factor-mediated disorder. It is also useful in assays
CC to determine biological activity, to raise antibodies, to isolate
CC corresponding ligands or receptors, to quantify levels of protein or
CC cognate corresponding ligand or receptors, as anti-inflammatory agents,
CC and in compositions for the treatment of skin, connective tissue and
CC immune system diseases. The polynucleotide is useful as marker for
CC tissue, as a chromosome marker or tags in the identification of a
CC genetic disorder.
XX
XX Sequence 529 AA:
SQ
Query Match 77.1%; Score 1371; DB 21; Length 529;
Best Local Similarity 93.4%; Pred. No. 3.4e-92;
Matches 255; Conservative 8; Mismatches 10; Indels 0; Gaps 0;
QY 50 PVSGDPPPLTMMTKDGTTHSGSRPRVLPQGLKWKOVEREDAGVYCKATNGFSLSVN 109
DB 48 PVSGDPPPLTMMTKDGTTHSGSRPRVLPQGLKWKOVEREDAGVYCKATNGFSLSVN 107
QY 110 YTLVLDLISPGKESLGPDSGGEDPASQOMARPRFTQPSKMRRVIRAPGSSVRLK 169
DB 108 YTLVLDLISPGKESLGPDSGGEDPASQOMARPRFTQPSKMRRVIRAPGSSVRLK 167
QY 170 CVASGHRPDIYWMKDQALTRPEAAEPRKKWTLKLNLRPEDSGKYTCRVSNRAGAIN 229
DB 168 CVASGHRPDIYWMKDQALTRPEAAEPRKKWTLKLNLRPEDSGKYTCRVSNRAGAIN 227
QY 230 ATYKVVIVQTRRSKPVLTGTHPVNTVVDGGTTSFOCKVRSVDKPVYIOMLKREYGAEGR 289
DB 228 ATYKVVIVQTRRSKPVLTGTHPVNTVVDGGTTSFOCKVRSVDKPVYIOMLKREYGAEGR 287
QY 290 HNSTIDVGOKFVLPDGTGWSRPDGSYLNRPL 322
DB 288 HNSTIDVGOKFVLPDGTGWSRPDGSYLNRPL 320
RESULT 9
AA019115
ID AA019115 standard; Protein; 439 AA.
XX
XX AAB19115;
XX
XX 19-FEB-2001 (first entry)
XX
XX Polypeptide isolated from lymph node stromal cells of fsn -/- mice.
XX

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```

KW Lymph node stromal cell; fsn -/- mice; inflammatory disorder;
KW immune system disorder; cancer; viral disorder; HIV infection;
KW blood vessel growth; tumour necrosis factor disorder; arthritis;
KW inflammatory bowel disease; fibroblast growth factor-mediated disorder;
KW cardiac failure.
XX
XX Mus sp.
XX
XX W0200058463-A1.
XX
XX 05-OCT-2000.
XX
XX 18-FEB-2000; 2000WO-NZ00015.
XX
XX 25-MAR-1999; 99US-0276268.
XX 26-AUG-1999; 99US-0383586.
XX
XX (GENE-) GENESIS RES & DEV CORP LTD.
XX Strachan L, Sleeman M, Abernethy N, Onrust R, Kumble KD;
PI Morrison JG;
XX WPI: 2000-664924/64.
XX N-PSDB; AAA96725.
DR
XX
XX Polypeptide expressed in mammalian fsn -/- lymph node stromal cells,
PT useful for modulating growth of blood cells, for treating inflammatory
PT and tumour necrosis factor-mediated disorders, cancer and viral
PT disorders
XX
XX Claim 1; Page 52-53; 75pp; English.
XX
XX The present sequence represents a polypeptide sequence which is
CC isolated from lymph node stromal cells of fsn -/- mice. The
CC polynucleotides and their polypeptides are useful for treating an
CC inflammatory disorder, disorder of immune system and cancer selected
CC from epithelial, lymphoid, myeloid, stromal and neuronal cancers, a
CC viral disorder, in particular HIV infection and for modulating the
CC growth of blood vessels. The polypeptides are useful for treating a
CC tumour necrosis factor (TNF) mediated disorder, such as those selected
CC from arthritis, inflammatory bowel disease and cardiac failure and a
CC fibroblast growth factor-mediated disorder. It is also useful in assays
CC to determine biological activity, to raise antibodies, to isolate
CC corresponding ligands or receptors, to quantify levels of protein or
CC cognate corresponding ligand or receptors, as anti-inflammatory agents,
CC and in compositions for the treatment of skin, connective tissue and
CC immune system diseases. The polynucleotide is useful as marker for
CC tissue, as a chromosome marker or tags in the identification of a
CC genetic disorder.
XX
XX Sequence 439 AA:
SQ
Query Match 57.8%; Score 1029; DB 21; Length 439;
Best Local Similarity 93.7%; Pred. No. 2.4e-67;
Matches 194; Conservative 4; Mismatches 9; Indels 0; Gaps 0;
QY 116 DOIISPGKESLGPDSGGEDPASQOMARPRFTQPSKMRRVIRAPGSSVRLKCVASGH 175
DB 23 DOIISPGKESLGPDSGGEDPASQOMARPRFTQPSKMRRVIRAPGSSVRLKCVASGH 82
QY 176 PRPDIYWMKDQALTRPEAAEPRKKWTLKLNLRPEDSGKYTCRVSNRAGAINATYKVD 235
DB 83 PRPDIYWMKDQALTRPEAAEPRKKWTLKLNLRPEDSGKYTCRVSNRAGAINATYKVD 142
QY 236 VIQTRRSKPVLTGTHPVNTVVDGGTTSFOCKVRSVDKPVYIOMLKREYGAEGRHNSTD 295
DB 143 VIQTRRSKPVLTGTHPVNTVVDGGTTSFOCKVRSVDKPVYIOMLKREYGAEGRHNSTD 202
QY 296 VGGOKFVLPDGTGWSRPDGSYLNRPL 322
DB 203 VGGOKFVLPDGTGWSRPDGSYLNRPL 229

```

RESULT 10  
AAM25511  
ID AAM25511 standard; Protein: 365 AA.  
XX  
AC AAM25511;  
XX  
DT 16-OCT-2001 (first entry)  
XX  
DE Human protein sequence SEQ ID NO:1026.  
XX  
KW Human; cancer; ulcer; HIV infection; human immunodeficiency virus;  
KW antiinflammatory; antirheumatic; antiarthritic; immunosuppressive;  
KW antibacterial; endocrine; cardiac; central nervous system; virucide;  
KW anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; anaemia;  
KW antiaggregant; haemostatic; vulnery; antilucer; osteopathic; eczema;  
KW dermatological; antiallergic; antiasthmatic; antidiabetic; cytosstatic;  
KW neuroprotective; antidepressant; nootropic; antiparkinsonian; infection;  
KW immunostimulant; gene therapy; antisense therapy; vaccine; inflammation;  
KW antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis;  
KW cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity;  
KW genetic disease; haematopoietic disorder; platelet disorder; asthma;  
KW thrombocytopaenia; osteoporosis; severe combined immunodeficiency;  
KW allergic rhinitis; diabetes; multiple sclerosis; depression;  
KW Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;  
KW neurological disorder.  
XX  
OS Homo sapiens.  
XX  
PN MO200153455-A2.  
XX  
PD 26-JUL-2001.  
XX  
PE 22-DEC-2000; 2000WO-US35017.  
XX  
PR 23-DEC-1999; 99US-0471275.  
PR 21-JAN-2000; 2000US-0488725.  
PR 25-APR-2000; 2000US-0552317.  
XX  
PA (HYSE-) HYSEQ INC.  
XX  
PI Tang YT, Liu C, Drmanac RT;  
XX  
DR WPI: 2001-457603/49.  
DR N-PSDB: AAM99452.  
XX  
PT Isolated human polynucleotides encoding polypeptides, useful for the  
XX treatment and diagnosis of e.g. cancer, ulcers and HIV infection -  
XX  
PS Claim 20; Page 210; 1217pp; English.  
XX  
CC AAM99166 to AAM99904 encode the human proteins given in AAM25225 to  
CC AAM25963. The proteins can have activities based on the tissues and  
CC cells they are expressed in, such as: antiinflammatory; antirheumatic;  
CC antiarthritic; immunosuppressive; antibacterial; endocrine; cardiac;  
CC central nervous system; virucide; anti-HIV; fungicide; antilucer;  
CC cardiovascular; antianaemic; antiaggregant; haemostatic; vulnery;  
CC antilucer; osteopathic; dermatological; antiallergic; antiasthmatic;  
CC antidiabetic; cytosstatic; neuroprotective; antidepressant; nootropic;  
CC antiparkinsonian; and immunostimulant. The proteins and polynucleotides  
CC encoding them can be used in gene therapy, antisense therapy and vaccine  
CC production. The proteins and polynucleotides are useful for screening for  
CC agonists or antagonists of a protein and for the treatment and diagnosis  
CC of disorders associated with the activity of a protein e.g. inflammation,  
CC rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction,  
CC neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal  
CC infections, autoimmunity, genetic diseases, haematopoietic disorders,  
CC anaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers,  
CC osteoporosis, severe combined immunodeficiency, eczema, allergic  
CC rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression,  
CC Alzheimer's disease, Parkinson's disease, neurodegenerative and  
CC neurological disorders.  
XX

SQ Sequence 365 AA;  
Query Match 57.3%; Score 1019; DB 22; Length 365;  
Best Local Similarity 99.5%; Pred. No. 1e-66;  
Matches 192; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 130 SSGGQEDPASOOWARPRTOPSKMRRVYARVGSVRLKCVASGHPRPDITMMKDDAL 189  
DB 5 ssggqedpasqwarprltqpskmrrvlarpgvssvrlkcvasghprpdlmddqdl 64  
QY 190 TRPEAAEPKRRKKWTLSTLKNLRPEDSGKTYTCRVSNAGA1NATYKVDVIOFTRSKPEVLGT 249  
DB 65 trpeaepkrkkwltslknlrpedsgkytcrvsnaganaikykvdiqtrtskpligt 124  
QY 250 HPVNTVDFGCTSFQCKVRSDVKPVIOMLKREYEGABGRNSTIDVGQKRVVLPFGDV 309  
DB 125 hpvntvdfgctsfqckvrsdvkpvigwlvkrveygaegrhnstldvggqkfvlpfgdv 184  
QY 310 WSRPDGSYLNRPL 322  
DB 185 wsrpdgsylnrpl 197  
RESULT 11  
AAM40429  
ID AAM40429 standard; Protein: 371 AA.  
XX  
AC AAM40429;  
XX  
DT 22-OCT-2001 (first entry)  
XX  
DE Human polypeptide SEQ ID NO 5360.  
XX  
KW Human; nootropic; immunosuppressant; cytosstatic; gene therapy; cancer;  
KW peripheral nervous system; neuropathy; central nervous system; CNS;  
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;  
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;  
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;  
KW leukaemia.  
XX  
OS Homo sapiens.  
XX  
PN MO200153312-A1.  
XX  
PD 26-JUL-2001.  
XX  
PE 26-DEC-2000; 2000WO-US34263.  
XX  
PR 21-JAN-2000; 2000US-0488725.  
PR 25-APR-2000; 2000US-0552317.  
PR 09-JUL-2000; 2000US-0598042.  
PR 19-JUL-2000; 2000US-0620312.  
PR 03-AUG-2000; 2000US-0653450.  
PR 14-SEP-2000; 2000US-0662191.  
PR 19-OCT-2000; 2000US-0693036.  
PR 29-NOV-2000; 2000US-0727344.  
XX  
PA (HYSE-) HYSEQ INC.  
XX  
PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;  
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;  
PI Zhao QH, Zhou P, Goodrich R, Drmanac RT;  
XX  
DR WPI: 2001-442253/47.  
DR N-PSDB: AAI59585.  
XX  
CC Novel nucleic acids and polypeptides, useful for treating disorders  
XX such as central nervous system injuries -  
XX  
PS Example 2; SEQ ID NO 5360; 10078pp; English.  
XX  
CC The invention relates to human nucleic acids (AA157798-AA161369) and

DR	N-PSDB; AAF16534.
XX	
PT	Prostate cancer associated gene sequences, referred to as prostate
PT	cancer antigens, useful for treatment, prevention, and diagnosis of
PT	disorders such as prostate cancer -
PS	
XX	
XX	Claim 11; Page 2183; 2338pp; English.
CC	
AAFI5566	to AAFI6505 encode the human prostate cancer associated
CC	proteins, called prostate cancer antigens, given in AAB56363 to AAB57302.
CC	The prostate cancer antigens can have neuroprotective, cytosolic,
CC	cardioactive, immunomodulatory, muscular, vlnary, gastrointestinal,
CC	nephrotropic, antiinfective, gynecological and antibacterial activities,
CC	and can be used in gene therapy. The prostate cancer antigen
CC	polynucleotides may be used for detection of prostate cancer. antigen
CC	identification, as chromosome markers, and for numerous other diagnostic
CC	or research purposes. The prostate cancer antigens may be used to treat
CC	disorders such as neural, immune, muscular, reproductive,
CC	gastrointestinal, pulmonary, cardiovascular, renal, and proliferative
CC	disorders, wounds, and infectious diseases. AAF16506 to AAF16514 to
CC	AAB57303 represent sequences used in the exemplification of the present
CC	invention.
XX	
SQ	Sequence 101 AA;
Query Match	29.7%; Score 529; DB 21; Length 101;
Best Local Similarity	99.0%; Pred. No. 1.3e-31;
Matches 99; Conservative	1; Mismatches 0; Indels 0; Gaps 0;
OY	171 VASGHPREDITWMKDDQALTREPAEAPRRKKWTLSLKNLRPDSKRYTCRVSNRAGATNA 230
Db	1 vassghprdiatwmkddqaltrepaeprrkkwtlslnlrpedsgkytcrvsnragaina 60
OY	231 TYKVADVIORTRSKPVLGTGNHNVNTVDVGGTSPQCKXYS 270
Db	61 tykvadvigrtskrpvlgtgnhnpvtlvdvggtstsqckxvrl 100
RESULT 13	
AAU02951	
ID	AAU02951 standard; Protein; 389 AA.
AC	AAU02951;
DT	12-SEP-2001 (first entry)
DE	Angiotensin converting enzyme (ACEV) splice variant protein #51.
XX	
XX	Angiotensin converting enzyme splice variant; ACEV; interleukin 6;
KW	granulocyte colony stimulating factor receptor; glucagon; hypertrophy;
KW	platelet-derived endothelial cell growth factor; cardiovascular disease;
KW	cellular tumor antigen P53; cyclin-dependent kinase inhibitor 1C;
KW	vasoactive intestinal polypeptide receptor 2; arteriosclerosis; cancer;
KW	myocardial infarction; coronary arterial thrombosis; renal disease;
KW	diabetic nephropathy; muscular disease; immune disorder; sarcoidosis;
KW	multiple sclerosis; immune complex nephritis; deep vein thrombosis;
KW	nonarcoidotic pulmonary granulomatous disease; endothelial abnormality;
KW	vascular disorder; asbestosis.
XX	
OS	Homo sapiens.
PN	WO200136632-A2.
XX	
PD	25-MAY-2001.
XX	
PB	17-NOV-2000; 200OWO-IL00766.
XX	
PR	17-NOV-1999; 99IL-0132978.
PR	10-DEC-1999; 99IL-0133455.
XX	
XA	(COMP-) COMPUGEN LTD.
XX	



[illegible][illegible]



Db 35 peepptkyqi-----sgpevyvaaggesleivrcllkdaavistwkdg--vhlgnpr 84  
 QY 76 RVL-POGLKQYEREDAGYVCKATNGFGLSNVNTLVLDISPEKESIGPDSSGGQ 134  
 Db 85 tllgeylqikgatrptisglyactastvdselwfmvntvdaisgdd----edddga 140  
 QY 135 EDPA5Q---QWAPRFPTQPSKRRRVIARPVSSVRLKCVASGHPRPDITWMDQALF- 190  
 Db 141 edfvsensnkrpypvntekmekrlhvaantvktfcpcagpmpmtumtvlknqkefkq 200  
 QY 191 --RPEAAEPKKKWTLSLKNLRPEDSKGYTCRVSNRAGAINATYKVDTORTSKPVLTG 248  
 Db 201 ehrtgykfvnqnqlwslimesvpsdkgnlcvvenegyslnhtyhlldversphrpilga 260  
 QY 249 THPNTVVDGCGTTSFQCKYRSQDVKYIOWLKRYE-----YGAGS-----RHNSITDV 296  
 Db 261 glpenastvvvgdvetrckvysdaqphlqwlkvhekngskypqdlpylklvklhsg---1 317  
 QY 297 GGQKFVVLPTGVDWSRPDSYLNK 320  
 Db 318 nsrnaevlalfnvteadageyick 341

## RESULT 17

AAR39647  
 ID AAR39647 standard; protein; 816 AA.

XX AAR39647;  
 AC

XX 14-JAN-1994 (first entry)  
 DT

XX Human fibroblast growth factor receptor.  
 DE

XX soluble; FGF-R; fibroblast growth factor receptor; tumour therapy;  
 KW immunoglobulin-like domain; tyrosine kinase activity; hyperplasia;  
 KW psoriasis; Herpes Simplex Virus; HSV.  
 XX

OS Homo sapiens.  
 XX

XX Key Location/Qualifiers  
 FH

FT Cleavage-site 21..22 /note= "putative signal peptidase site"  
 FT

FT Domain 55..101 /label= Ig-like\_domain\_1  
 FT

FT Domain 179..231 /label= Ig-like\_domain-2  
 FT

FT Domain 278..341 /label= Ig-like\_domain-3  
 FT

FT Region 126..133 /label= AR  
 FT

FT /note= "acidic amino acid rich region"  
 FT

FT Misc-difference 137..143 /note= "the sequence EEKKEKE in Seq.ID.No.1 is  
 FT shown as EEKE in Fig. 2"  
 FT

FT Domain 372..392 /label= 8 transmembrane  
 FT

FT Domain 475..575 /label= "Tyrosine\_kinase\_domain  
 FT /note= "first part of split TK domain"  
 FT

FT Domain 590..750 /label= "Tyrosine\_kinase\_domain  
 FT /note= "second part of split TK domain"  
 FT

XX US5229501-A.  
 PN

XX 20-JUL-1993.  
 PD

XX 11-JAN-1991; 91US-0640029.  
 PF

XX 11-JAN-1991; 91US-0640029.  
 PR

XX (CHIR ) CHIRON CORP.  
 PA

XX

PI Barr PJ, Kelfer MC, Valenzuela PDR;  
 XX  
 DR WPI; 1993-242535/30.  
 XX  
 PT New recombinant human fibroblast growth factor receptor - is  
 PT useful in treatment of hyperplasia(s), tumours and herpes simplex  
 PT infection  
 XX  
 PS Claim 1; Fig 2 and Columns 13-18; 21pp; English.  
 XX  
 CC The invention covers both the full-length FGF-receptor and its  
 CC soluble form (i.e. truncated by deletion of the C-terminal portion  
 CC beginning at the transmembrane domain). The FGF receptor is defined  
 CC as having the sequence in Columns 13-18 and Fig 2. These sequences  
 CC differ slightly as indicated by the "Misc.difference" in the  
 CC features table. The receptor can be used to detect FGF or to inhibit  
 CC FGF activity. Specifically, the soluble form of the receptor can  
 CC inhibit FGF-dependent tumour growth, angiogenesis, psoriasis,  
 CC excessive scar formation and hyperplasias and can be used to treat  
 CC Herpes Simplex virus infections.  
 CC  
 SQ Sequence 816 AA;

Query Match 21.0%; Score 373; DB 14; Length 816;  
 Best Local Similarity 30.1%; Pred. No. 3.1e-19;  
 Matches 89; Conservative 46; Mismatches 115; Indels 46; Gaps 8;

QY 20 RPPF--PEAPQWRTRMSHGCRPAGPCAAAVPEG-----DPPPLTMW 61  
 Db 22 rpsplclpegaqpw-----gapvevesflvhpqdlqlrcrlrdvgslnw 66  
 QY 62 TKDGRTHSGMSRRRVLPOGLKQYEREDAGYVCKATNGFGLSNVNTLVLDISPG 121  
 Db 67 lrdvgqlaes-ntrltgeevvqdsvpadsqglyactsspsgs-dtltyisvnsdals 124  
 QY 122 KESLGPSSSGGQE-----DPASQOMARPRFTQPSKRRRVIARPVSSVRLKCVASGH 175  
 Db 125 seddddddssseekkeketndtknprvayrwtsepkmekrlhvaantvktfcpcssgt 184  
 QY 176 PRPDITWMDQALTRPE---AAEPKKKWTLSLKNLRPEDSKGYTCRVSNRAGAINAT 231  
 Db 185 pncflrwlknqkef-kpdrtygykvatwsilmdsvpsdkgnlcvvenegyslnht 243  
 QY 232 YKVNVIGRTKSKRVLTGTHPNTVVDGCGTTSFQCKYRSQDVKYIOWLKRYEAGAE 287  
 Db 244 yqldvversphrpilqaglpanktvalgsnvelmckvysdpqphlqwlkhlewsk 299

## RESULT 18

AAR15268  
 ID AAR15268 standard; protein; 769 AA.

XX AAR15268;  
 AC

XX 18-FEB-1992 (first entry)  
 DT

XX Clone pTBI284-encoded complete FGF receptor.  
 DE

XX Human; fibroblast growth factor; cancer.  
 KW

XX Homo sapiens.  
 OS

XX WO9117183-A.  
 PN

XX 14-NOV-1991.  
 PD

XX 25-APR-1991; 91WO-JP00557.  
 PF

XX 28-DEC-1990; 90JP-0415801.  
 PR

XX 27-APR-1990; 90JP-0113146.  
 PR

XX 31-JUL-1990; 90JP-0204438.  
 PR

XX 14-SEP-1990; 90JP-0245256.  
 PR

XX (TAKE ) TAKEDA CHEMICAL IND KK.  
 PA Igarashi K, Senoo M, Watanabe T;  
 XX WPI, 1991-353723/48.  
 DR N-PSDB; AAQ14268.  
 XX  
 PT New mutin(s) of proteins - with fibroblast growth factor  
 PT receptor activity, useful for treating multiple endocrine  
 PT neoplasia, prostatic hypertrophy, used for diagnosis  
 PS  
 PS Example 3; Fig 7; 88pp; English.  
 CC A cDNA library prepared from human cancer cell line Kato III mRNA  
 CC was screened with an oligonucleotide corresponding to amino acids  
 CC 529-541 of chicken basic FGF receptor. Three positive clones were  
 CC obtained. One was cloned into pUC18/119 to give pPB1229 (see  
 CC AAQ14849). The complete FGF coding sequence was obtained by ligating  
 CC the insert from pPB1229 to the DNA sequence of the plasmid pPB1281  
 CC insert which encodes the carboxyl terminus of the FGF receptor from  
 CC Glu 533 onwards.  
 XX  
 SQ Sequence 769 AA;  
 Query Match 20.9%; Score 371.5; DB 12; Length 769;  
 Best Local Similarity 29.6%; Pred. No. 3.7e-19;  
 Matches 96; Conservative 56; Mismatches 129; Indels 43; Gaps 10;  
 QY 23 PPEAPORWRTKRWGHPAGPHCAAVPYEG-----DPPPLTMTKDGRTIHSGWSRP 75  
 DB 35 peepptkkyqf-----sqpevyvaageslevrcllkdaavlswtckdg--vhlgnmr 84  
 QY 76 RVL-POGLKVKQVERDAGYVVCATNGFGLSVNTLVLDISPGKEELGPDSSSGQ 134  
 DB 85 tvllgeyqlqkgaetprdsqlyactastvdselwfmvntdaissgd-----edtdga 140  
 QY 135 EDPASQ---QWAPRFTQPSKMRRIYARVPGSSVRLKCVASGHPRPDITWMDQALT- 190  
 DB 141 edfvsensnmkrpwtntekmekrlhavpaantvfcrcpagnpmpmtwlnkgefkq 200  
 QY 191 --RPEAAEPKKKWTLSLKNLRPDSGKTYTCRVSNRAGAINATYKYDVIORTSKPYLTG 248  
 DB 201 ehrlggykvrynghwslimevsvpsekgytccveneygsinhylhdiversphrpilga 260  
 QY 249 THEVNTTVDGCTTSFOCKVRSVVKPVIOWLKRYE-----YGAEG-----RHNSTIDV 296  
 DB 261 glpnaastlvvgdvelfvckvysdaqphlqwlkiveknsgkysgpdglpylklvkhsg--1 317  
 QY 297 GGGKFVVLPTGDVWSRPDSGLNK 320  
 DB 318 nssnaevlalfnvteadageyick 341  
 RESULT 19  
 AAR21080  
 ID AAR21080 standard; protein; 821 AA.  
 XX AAR21080;  
 AC AAR21080;  
 XX  
 DT 20-MAY-1992 (first entry)  
 XX  
 DE flg receptor protein.  
 XX  
 KW Fibroblast growth factor receptor; heparin binding proteins;  
 KW tyrosine kinase; bacterially expressed kinase; CSF-1; PDGF.  
 XX  
 OS Homo sapiens.  
 XX  
 FH key Location/Qualifiers  
 FT Peptide 1..21  
 FT /label= signal\_peptide

FT Protein 22..821  
 FT /label= bek\_receptor\_protein  
 FT  
 PN WO9200999-A.  
 XX  
 PD 23-JAN-1992.  
 XX  
 PF 03-JUL-1991; 91WO-US04745.  
 XX  
 PR 06-JUL-1990; 90US-0549587.  
 XX  
 PA (RORER ) RORER INT HOLDINGS.  
 PI Dione CA, Crumley G, Jaye MC, Schlessinger J;  
 DR WPI, 1992-056827/07.  
 DR N-PSDB; AAQ21003.  
 XX  
 PT New fibroblast growth factor receptor proteins - useful in  
 PT treating GF-mediated conditions e.g. angiogenesis of tumours,  
 PT mitogenic effects in psoriasis, arthritis  
 PS  
 PS Claim 5; Fig 8; 65pp; English.  
 CC The protein sequence was deduced from the DNA sequence of an flg  
 CC cDNA clone having increased binding for aFGF receptors. Flg and bek  
 CC are similar but distinct gene products with structural features shared  
 CC by the PDGF/CSF-1/c-Kit family of receptor linked tyrosine kinases.  
 CC They have a 21 residue hydrophobic signal sequence, bek has an  
 CC extracellular domain of 356 residues and a cytoplasmic domain of 423  
 CC residues. The extracellular domain contains 3 "immunoglobulin like"  
 CC domains of similar size and location. There are eight potential  
 CC N-glycosylation sites. There is an "acidic box" of 5 amino acids.  
 CC The cytoplasmic domain consists of long juxtamembrane regions followed  
 CC by catalytic kinase domains which are split by 14 amino acid insertions.  
 CC The kinase domains are followed by divergent carboxy terminal tails.  
 CC Receptor proteins encoded by this cDNA sequence may be used in pharm-  
 CC aceutical compns. to inhibit undesirable heparin-binding growth factor  
 CC mediated cellular responses or to inhibit the binding of an  
 CC opportunistic pathogen to human cells. Such undesirable responses may be  
 CC growth factor stimulated angiogenesis and vascularisation of tumours,  
 CC mitogenic effects in psoriasis, arthritis, atherosclerosis and benign  
 CC prostatic hyper- trophy. The derived flg protein may also be used for  
 CC screening drugs for treatment of such problems.  
 CC See also AAR20750.  
 XX  
 SQ Sequence 821 AA;  
 Query Match 20.9%; Score 371.5; DB 13; Length 821;  
 Best Local Similarity 31.6%; Pred. No. 4e-19;  
 Matches 90; Conservative 50; Mismatches 112; Indels 33; Gaps 8;  
 QY 23 PPEAPORWRTKRWGHPAGPHCAAVPYEG-----DPPPLTMTKDGRTIHSGWSRP 75  
 DB 35 peepptkkyqf-----sqpevyvaageslevrcllkdaavlswtckdg--vhlgnmr 84  
 QY 76 RVL-POGLKVKQVERDAGYVVCATNGFGLSVNTLVLDISPGKEELGPDSSSGQ 134  
 DB 85 tvllgeyqlqkgaetprdsqlyactastvdselwfmvntdaissgd-----edtdga 140  
 QY 135 EDPASQ---QWAPRFTQPSKMRRIYARVPGSSVRLKCVASGHPRPDITWMDQALT- 190  
 DB 141 edfvsensnmkrpwtntekmekrlhavpaantvfcrcpagnpmpmtwlnkgefkq 200  
 QY 191 --RPEAAEPKKKWTLSLKNLRPDSGKTYTCRVSNRAGAINATYKYDVIORTSKPYLTG 248  
 DB 201 ehrlggykvrynghwslimevsvpsekgytccveneygsinhylhdiversphrpilga 260  
 QY 249 THEVNTTVDGCTTSFOCKVRSVVKPVIOWLKRYE-----YGAEG 288  
 DB 261 glpnaastlvvgdvelfvckvysdaqphlqwlkiveknsgkysgpdg 305



XX Novel fusion protein constructs comprise a fibroblast growth factor (FGF) receptor (FGF-R) extracellular domain (ECD) lacking the immunoglobulin (Ig) I segment fused to a heterologous oligomerization domain that comprises an immunoglobulin Fc region, hinge region, CH1, CH2, CH3 or CH4 region, or light chain of an immunoglobulin molecule, or a peptide with a leucine zipper motif. The Ig I segment is not necessary for binding of acidic FGF and basic FGF (bFGF). The Ig I deletion further increases the affinity for aFGF and heparin, protects the core of the molecule from proteolysis, and abrogates the heparin requirement for aFGF binding. The new fusion polypeptides are better FGF inhibitors than FGF-R monomer proteins. The FGF-R-Ig Fc fusion dimers are active as FGF antagonists at subnanomolar concentrations and were 20-fold more potent than the FGF-R monomer protein as competitors of bFGF binding to immobilized FGF-Rs. The fusion constructs are useful to treat FGF-, angiogenesis-, or FGF-R-mediated disorders, such as tumorigenesis (e.g. bladder, breast, lung, rectal, testis and cervical tumors), neovascularization (e.g. diabetic retinopathy, neovascular glaucoma), wound healing and corneal scarring) and hyper-proliferation of vascular smooth muscle cells (e.g. postangioplasty and postatherectomy restenosis).

XX Sequence 622 AA:

Query Match 20.5%; Score 364.5; DB 21; Length 622;  
Best Local Similarity 30.4%; Pred. No. 9, 4e-19;  
Matches 88; Conservative 43; Mismatches 115; Indels 43; Gaps 8;

OY 20 RPP--PEAPQRMRTMSHGMPAGPHCAAVVEG-----DPPPLTMW 61  
DB 22 rpsrlpbeqagpw-----gapvevesflvhpqdlqlrcrlrdvgslnw 66  
OY 62 TKDGRTHSGMSRFRVLPQGLKQYEREDAGYVCKATNGFSLSVNTLVLLDDISPG 121  
DB 67 lrdgvglaes-ntrltgveevqdvspadsglyacvtspgs-dtyfsvnsdalps 124  
OY 122 KESLGPDDSSSGOE--DPASQOMARPRFTQPSKMRRTVYARVYGVSSVRLCYASGHRP 178  
DB 125 seddddddssseketdntkpnvavpawpyspekmecklnavpaaktvfkcpssgtpp 184  
OY 179 DITWMDDDQALTRPE----AAERPKKKWTLISLKNLRPDSGKTCYVSNRAGAINATYKV 234  
DB 185 tlrlwkngrkef-kpdmrlggykvryatwslnmsvpsdkgnytlciveneyslnhtyql 243  
OY 235 DVIOFRSRKPVLTGTHPVNTTVDGFGTSPQCKRSDVVKVRLKRV 283  
DB 244 dvversphrpilqaglpanktvalgsnveimckvysdpqphiqwkhie 292

RESULT 22

AA47233  
ID AA47233 standard; Protein; 820 AA.

XX AA47233;

XX 07-SEP-1994 (first entry)

XX Human fibroblast growth factor receptor.

XX Cytomegalovirus; CMV; Towne; gH gene; escort protein;  
KW recombinant protein production; viral glycoprotein H; FGF receptor;  
KW fibroblast growth factor receptor; soluble; flg5 cDNA clone.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Peptide 1..21

XX Protein 22..820

XX Domain /label= human\_FGF\_receptor

XX /label= immunoglobulin-like\_domain\_1

XX /note= "extracellular"

FT Domain 176..228  
FT /label= immunoglobulin-like\_domain\_2  
FT /note= "extracellular"  
FT Domain 275..339  
FT /label= immunoglobulin-like\_domain\_3  
FT /note= "extracellular"  
FT Region 126..133  
FT /label= ARR  
FT /note= "acidic amino acid-rich region"  
FT Domain 374..395  
FT /label= transmembrane\_domain  
FT Domain 478..578  
FT /label= TK  
FT /note= "first part of split intracellular tyrosine kinase domain"  
FT Domain 593..754  
FT /label= TK  
FT /note= "second part of split intracellular tyrosine kinase domain"

PN WO9403620-A.

PD 17-FEB-1994.

PF 29-JUL-1993; 93WO-US07299.

PR 29-JUL-1992; 92US-0921807.

XX (CHIR ) CHIRON CORP.

XX Spaete RL;

XX WPI; 1994-065708/08.

PT Increased expression and secretion of viral protein e.g. from  
PT cytomegalovirus from host cells - by co-expression with DNA  
PT encoding an escort protein, e.g. fibroblast growth factor  
PT receptor

PS Claim 8; Fig 6; 86pp; English.

XX Expression of recombinant viral glycoproteins on host cell surfaces  
CC can be significantly enhanced by coexpression with an escort  
CC protein. The CMV glycoprotein H polypeptide (see AA47232) is a  
CC preferred viral glycoprotein and is pref. coexpressed with human  
CC fibroblast growth factor receptor. A full-length FGF receptor cDNA,  
CC designated flg5, was isolated from a lambda ZAP human hepatoma  
CC HepG2 cDNA library; flg5 codes for a 820 amino acid protein having  
CC the sequence AA47233.

XX Sequence 820 AA:

Query Match 20.5%; Score 364.5; DB 15; Length 820;  
Best Local Similarity 30.4%; Pred. No. 1, 3e-18;  
Matches 88; Conservative 43; Mismatches 115; Indels 43; Gaps 8;

OY 20 RPP--PEAPQRMRTMSHGMPAGPHCAAVVEG-----DPPPLTMW 61

DB 22 rpsrlpbeqagpw-----gapvevesflvhpqdlqlrcrlrdvgslnw 66

OY 62 TKDGRTHSGMSRFRVLPQGLKQYEREDAGYVCKATNGFSLSVNTLVLLDDISPG 121

DB 67 lrdgvglaes-ntrltgveevqdvspadsglyacvtspgs-dtyfsvnsdalps 124

OY 122 KESLGPDDSSSGOE--DPASQOMARPRFTQPSKMRRTVYARVYGVSSVRLCYASGHRP 178

DB 125 seddddddssseketdntkpnvavpawpyspekmecklnavpaaktvfkcpssgtpp 184

OY 179 DITWMDDDQALTRPE----AAERPKKKWTLISLKNLRPDSGKTCYVSNRAGAINATYKV 234

DB 185 tlrlwkngrkef-kpdmrlggykvryatwslnmsvpsdkgnytlciveneyslnhtyql 243





## ALIGNMENTS

## RESULT 1

US-09-383-586-33  
Sequence 33, Application US/09383586  
Patent No. 6242419

## GENERAL INFORMATION:

APPLICANT: Strachan, Lorna  
APPLICANT: Sleeman, Matthew  
APPLICANT: Abernethy, Nevlin  
APPLICANT: Ormest, Rene  
APPLICANT: Kumble, Anand  
APPLICANT: Murison, Greg

TITLE OF INVENTION: Compounds isolated from stromal cells  
FILE REFERENCE: 11000.1037c1  
CURRENT APPLICATION NUMBER: US/09/383,586  
CURRENT FILING DATE: 1999-08-26  
NUMBER OF SEQ ID NOS: 38  
SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 33  
LENGTH: 322  
TYPE: PRT  
ORGANISM: Human

US-09-383-586-33

Query Match  
Best Local Similarity 100.0%; Score 1779; DB 4; Length 322;  
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRAPCCSCCRRCMBSPRRPPRRPQRRRRMSGRNPGHCAANVPEBPPPLTM 60  
DB 1 RRAPCCSCCRRCMBSPRRPPRRPQRRRRMSGRNPGHCAANVPEBPPPLTM 60  
QY 61 WTKDGRTHSGMSRFRVLPQGLKVKQVEREDAGVYCKATNGSGSVNTLVLDISP 120  
DB 61 WTKDGRTHSGMSRFRVLPQGLKVKQVEREDAGVYCKATNGSGSVNTLVLDISP 120  
QY 121 GKESLGPDSGGQEDPASQOMARPRFTOPSKRRRVIAAPVGSVRLKCVASGHRPDI 180  
DB 121 GKESLGPDSGGQEDPASQOMARPRFTOPSKRRRVIAAPVGSVRLKCVASGHRPDI 180  
QY 181 TWMKDDQALTRPEAAEPKRRKWTLSLKNLRPDSGKYTCRVSNRAGAINATYKVDYQRT 240  
DB 181 TWMKDDQALTRPEAAEPKRRKWTLSLKNLRPDSGKYTCRVSNRAGAINATYKVDYQRT 240  
QY 241 RSKPVLGTGHPVNTVDFGGTSPQCKVRSADVAPVYQMLKRYEYGAEGHNSTIDVGOK 300  
DB 241 RSKPVLGTGHPVNTVDFGGTSPQCKVRSADVAPVYQMLKRYEYGAEGHNSTIDVGOK 300  
QY 301 FVVLPTGDVMSRPDGSYLKPL 322  
DB 301 FVVLPTGDVMSRPDGSYLKPL 322

## RESULT 2

US-09-383-586-31  
Sequence 31, Application US/09383586  
Patent No. 6242419

## GENERAL INFORMATION:

APPLICANT: Strachan, Lorna  
APPLICANT: Sleeman, Matthew  
APPLICANT: Abernethy, Nevlin  
APPLICANT: Ormest, Rene  
APPLICANT: Kumble, Anand  
APPLICANT: Murison, Greg

TITLE OF INVENTION: Compounds isolated from stromal cells  
FILE REFERENCE: 11000.1037c1

CURRENT APPLICATION NUMBER: US/09/383,586

CURRENT FILING DATE: 1999-08-26

NUMBER OF SEQ ID NOS: 38

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 31

LENGTH: 529

TYPE: PRT

ORGANISM: Mouse

US-09-383-586-31

Query Match  
Best Local Similarity 77.1%; Score 1371; DB 4; Length 529;  
Matches 255; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

QY 50 PVEGDPPPLTMWTKDGRTHSGMSRFRVLPQGLKVKQVEREDAGVYCKATNGSGSVN 109  
DB 48 PVEGDPPPLTMWTKDGRTHSGMSRFRVLPQGLKVKQVEREDAGVYCKATNGSGSVN 107  
QY 110 YTLVLDISPGRKESLGPDSGGQEDPASQOMARPRFTOPSKRRRVIAAPVGSVRLK 169  
DB 108 YTLVLDISPGRKESLGPDSGGQEDPASQOMARPRFTOPSKRRRVIAAPVGSVRLK 167  
QY 170 CVASGHRPDIWTKDDQALTRPEAAEPKRRKWTLSLKNLRPDSGKYTCRVSNRAGAIN 229  
DB 168 CVASGHRPDIWTKDDQALTRPEAAEPKRRKWTLSLKNLRPDSGKYTCRVSNRAGAIN 227  
QY 230 ATYKVDYQRTSKRPVLTGHPVNTVDFGGTSPQCKVRSADVAPVYQMLKRYEYGAEGR 289  
DB 228 ATYKVDYQRTSKRPVLTGHPVNTVDFGGTSPQCKVRSADVAPVYQMLKRYEYGAEGR 287  
QY 290 HNSTDVGOKFVVLPTGDVMSRPDGSYLKPL 322  
DB 288 HNSTDVGOKFVVLPTGDVMSRPDGSYLKPL 320

## RESULT 3

US-09-383-586-32  
Sequence 32, Application US/09383586  
Patent No. 6242419

## GENERAL INFORMATION:

APPLICANT: Strachan, Lorna  
APPLICANT: Sleeman, Matthew  
APPLICANT: Abernethy, Nevlin  
APPLICANT: Ormest, Rene  
APPLICANT: Kumble, Anand  
APPLICANT: Murison, Greg

TITLE OF INVENTION: Compounds isolated from stromal cells  
FILE REFERENCE: 11000.1037c1  
CURRENT APPLICATION NUMBER: US/09/383,586  
CURRENT FILING DATE: 1999-08-26  
NUMBER OF SEQ ID NOS: 38  
SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 32  
LENGTH: 439  
TYPE: PRT  
ORGANISM: Mouse

US-09-383-586-32

Query Match  
Best Local Similarity 57.8%; Score 1029; DB 4; Length 439;  
Matches 194; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY 116 DISPGKESLGPDSGGQEDPASQOMARPRFTOPSKRRRVIAAPVGSVRLKCVASGH 175  
DB 23 DISPGKESLGPDSGGQEDPASQOMARPRFTOPSKRRRVIAAPVGSVRLKCVASGH 82  
QY 176 PRPDITWTKDDQALTRPEAAEPKRRKWTLSLKNLRPDSGKYTCRVSNRAGAINATYKVD 235  
DB 83 PRPDITWTKDDQALTRPEAAEPKRRKWTLSLKNLRPDSGKYTCRVSNRAGAINATYKVD 142

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